

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: July 9, 2005, 11:30:14 ; Search time 43 Seconds
(without alignments)
1203.828 Million cell updates/sec

Title: US-10-620-169-4
Perfect score: 2958
Sequence: 1 MPRGWAEPLLLLLQGWGC.....YLRQWVPPPLSSPGQAS 538

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0
Maximum DB seq length: 2000000000
Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : PIR 79:*
1: pir1:*
2: pir2:*
3: pir3:*
4: pir4:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	278	9.4	531	2 A30342	interleukin-2 rece
2	249	8.4	537	2 B46535	interleukin-2 rece
3	247.5	8.4	539	2 A35052	interleukin-2 rece
4	233	7.9	896	1 A35782	cytokine receptor
5	221.5	7.5	468	2 A45268	interleukin-9 rece
6	218.5	7.4	878	1 A40091	interleukin-3 rece
7	215	7.3	522	2 B45268	interleukin-9 rece
8	213.5	7.2	467	2 I56896	gene gfi-2 protein
9	213	7.2	508	1 ZUHUR	erythropoietin rec
10	211.5	7.2	896	2 I56563	interleukin-3 rece
11	204	6.9	897	1 A39255	cytokine receptor
12	201	6.8	507	1 A32385	erythropoietin rec
13	195	6.6	507	1 A46713	erythropoietin rec
14	193.5	6.5	825	1 A60386	interleukin-4 rece
15	189.5	6.4	810	1 A33380	interleukin-4 rece
16	171	5.8	348	2 JC7907	common cytokine re
17	168.5	5.7	635	2 A45266	MPL-P protein prec
18	168.5	5.7	800	1 S31575	interleukin-4 rece
19	168	5.7	369	2 I49280	interleukin-2 rece
20	164.5	5.6	579	2 B45266	MPL-K protein prec
21	159	5.4	831	2 J01655	prolactin receptor
22	157	5.3	625	2 S35317	hematopoietic grow
23	157	5.3	626	2 S37622	proto-oncogene - m
24	151.5	5.1	805	2 S68441	leptin receptor, s
25	151.5	5.1	892	2 S68439	leptin receptor, s
26	151.5	5.1	894	2 S68437	leptin receptor, s
27	151.5	5.1	900	2 S68440	leptin receptor, s
28	151.5	5.1	1162	2 S68438	leptin receptor, s
29	146	4.9	459	2 A34791	interleukin-7 rece

30	144	4.9	373	2 A55718	interleukin-2 rece
31	143.5	4.9	459	2 D34791	interleukin-7 rece
32	143	4.8	369	2 A42565	interleukin-2 rece
33	139.5	4.7	298	2 B34791	interleukin-7 rece
34	139	4.7	895	2 S74225	leptin receptor, i
35	139	4.7	1162	2 PC4184	leptin receptor, O
36	135.5	4.6	954	1 S68178	mixed-lineage prot
37	128.5	4.3	284	2 S27931	Env/v-mpl fusion p
38	128.5	4.3	918	2 A44257	interleukin-6 sign
39	126.5	4.3	917	2 I49699	glycoprotein 130 -
40	125	4.2	262	2 C34791	interleukin-7 rece
41	123	4.2	295	2 A44984	collagen - nematod
42	123	4.2	468	1 A41242	interleukin-6 rece
43	123	4.2	1744	2 S40991	collagen alpha 1(I)
44	122.5	4.1	420	2 S21052	interleukin-5 rece
45	121.5	4.1	2124	2 A28452	proteoglycan core

ALIGNMENTS

RESULT 1

A30342
interleukin-2 receptor beta chain precursor - human
N:Alternate names: CD25 beta chain
C:Species: Homo sapiens (man)
C:Date: 31-Mar-1990 #sequence_revision 31-Mar-1990 #text_change 09-Jul-2004
C:Accession: A30342
R:Hatakeyama, M.; Tsudo, M.; Minamoto, S.; Kono, T.; Doi, T.; Miyata, T.; Miyasaka, M.;
Science 244, 551-556, 1989
A:Title: Interleukin-2 receptor beta-chain gene: generation of three receptor forms by
A:Reference number: A30342; MUID:89242117; PMID:2785715
A:Accession: A30342
A:Molecule type: mRNA
A:Residues: 1-551 <HAT>
A:Cross-references: UNIPROT:P14784; GB:M26062; NID:q186322; PIDN:AAA59143.1; PID:G307048
C:Genetics:
A:Gene: GDB:IL2RB
A:Cross-references: GDB:118822; OMIM:146710
A:Map position: 22q11.2-22q13
C:Superfamily: interleukin-2 receptor beta chain; fibronectin type III repeat homology
C:Keywords: cytokine receptor; transmembrane protein
F:1-26/Domain: signal sequence #status predicted <SIG>
F:27-551/Product: interleukin-2 receptor beta chain #status predicted <MAT>

Query Match	9.4%	Score 278;	DB 2;	Length 551;
Best Local Similarity	26.0%	Pred. No. 4.7e-12;		
Matches 137;	Conservative 75;	Mismatches 199;	Indels 116;	Gaps 31;
QY	5	WAAPLILL--LQGW-----GCPDLVCYTDYLTQTVICILEMNLHPSTLTLTWDDQVE	56	
Db	8	WRLPLLILLPLATSWASAAVNGTSQFTCFYNSRANISCV---WS-----QDG	52	
QY	57	ELKDEATSCSLH-----RSAHNAT-----HATYTCM-----DVPHFMADDFSVNITD	100	
Db	53	ALQD--TSCQVHAMPDRRRWNOTCELLPVSQASWACNLILGAPDSQKLTVDIVTLRLVC	110	
QY	101	OSGNYSORCG--SFLLAESIKPAPPFNVTVF--SGQYNISWRSDYEDPAFYLKGLQY	156	
Db	111	REGVWRVWATQDFKPFENLRMAPISLOVVHVEHRCNISWEI---SQASHYFERHLEF	167	
QY	157	ELQVNRGDPWAVGPRRKLISVDSRSVLLPLEFRKDSSEYELQVRAGMPGSSYQGTWSE	216	
Db	168	EARTLSPGHTWEEAP---LLTLKQKQEWICLETLPDQYEFQVRVKPLQGEF--TTWSP	222	
QY	217	WSDPVIPTQSEBELKEG---WNPHLLILLVIVIPAFWSL-----KTHPLWRLN-KKIW	268	
Db	223	WSQPLAFRTKPAALGKDTIPWLGHLLVGLSGAFGFIILVYLLINCNTGP-----WLKKYL	278	
QY	269	A--VSPSPREFMPLYKGCSDGPKWVGAPFTGSSLELGFMPGPEVPSTLEVYSHCHPRSPA	326	
Db	279	KNTPTDPSKFFQSLSSEHGGDVQKWLSSPFFSSPGLAPEI--SPLEV-----L	328	

cytokine receptor common beta chain precursor - mouse
C:Species: Mus musculus (house mouse)
C>Date: 30-Jun-1993 #sequence_revision 30-Jun-1993 #text_change 09-Jul-2004
C:Accession: A35782
R:Gorman, D.M.; Itoh, N.; Kitamura, T.; Schreurs, J.; Yonehara, S.; Yahara, I.; Arai, K.
Proc. Natl. Acad. Sci. U.S.A. 87, 5459-5463, 1990
A:Title: Cloning and expression of a gene encoding an interleukin 3 receptor-like protein
A:Reference number: A35782; MUID:90319131; PMID:1695379
A:Accession: A35782
A:Molecule type: mRNA
A:Residues: 1-896 <OR>
A:CROSS-references: UNIPROT:P26955; GB:M34397; NID:gl91821; PIDN:AAA37204.1; PID:g309101
C:Comment: Mouse high-affinity IL-5, GM-CSF, and one class of high-affinity IL-3 receptor
C:Superfamily: cytokine IL-3/IL-5/GM-CSF receptor common beta chain; cytokine receptor H
F:1-22/Domain: signal sequence #status predicted <SIG>
F:23-896/Product: cytokine receptor common beta chain #status predicted <EXT>
F:23-441/Domain: extracellular #status predicted <EXT>
F:39-235/Domain: cytokine receptor homology <CRS1>
F:253-434/Domain: cytokine receptor homology <CRS2>
F:442-463/Domain: transmembrane #status predicted <TM>
F:464-896/Domain: intracellular #status predicted <INT>

Query Match 7.9%; Score 233; DB 1; Length 896;
Best Local Similarity 20.4%; Pred. No. 1.3e-08;
Matches 113; Conservative 86; Mismatches 220; Indels 134; Gaps 23;
QY 22 DLVCTDYLQTVICILEMWN-----LHPSTLTLTQDQYEELKDEATSCSLHRS 70
DB 250 NLQCFDGLQSLHCSWEVWTTQTSVGLFVRPSVA-----PEEKCSFVVKPE 299
Q* 71 ANNATHATYCHMDVHFHMADIFSVNITDQSGNYSQEGSFLLA-ESIKAPP-FNVTV 128
DB 300 PGASVYTRYHCSLPPEPSAHSQYTVSVK-----HLEQKFIYSNHIQEPPTLNLT 353
QY 129 TFSQGNYSWSRDYEDPAPYMLKGLQYELQYLRNRPDPAVSPRKLISVDSRSVLLPL 188
DB 354 N-RDSYLSHWETQKWAYSFI-----BHTFQVQYKKSQSDSWEDSKTENLDRAHSMDS 404
QY 189 EPRKDSYELQVRAGPMFGSSYQGTWSEWSDVIFQTSSEELKEGWNPHLLILLVIVF 248
DB 405 QLEPDTSYCARVRKPI--SNYDGIWSKWESEYTKT-DWVPTLWVILLVFLITLL 461
QY 249 IPAFWSLTHPLWRLKWKIWAIVSPERFPMPLYKCGSGDFKKWGAPFTGSSLELGPWSP 308
DB 462 ILRFQGVSYRYRKWKE--KIPNPSKSL-----FQDGGKGLWP--- 499
QY 309 EYPSLEYVYCHPP--RSPAKQLQTELOEPAELVESDGVKPSFWPTAQNSGGSAYSEE 366
DB 500 --PGSMAAFATKPNALQGPQSL-LAEQQ-----GESSYHL 532
QY 367 RDRPYGLVSDIVTVL--DAEGPCTWPCSD--DGYPALDLDAGLEPSPGLDPLLDAG 422
DB 533 EDNVSPLTIEDPIIRVPPSGDTPPAASSESTQLPNVQEGTTPNRPKQLSPD-- 590
QY 423 TTVLSCGCVSAGSPGLGGP-----LGLSLDLRLKPLADGE--DWAGGLPWGRSPG-- 472
DB 591 -----FNGPYLGPQSHSLPDLPLQSGSPQVGGSLKPLPGSLEYMCLAPGQVQ 640
QY 473 -----VSEESAGSPLAGLMDTDFSGFVGSDCSPVECDFTSPGDEGPPRSYLROWVV 525
DB 641 LVPLSQVMGQGMADVQCGSSLETSGSPVEKPNPVELSMEEQEARNDP----- 691
QY 526 IPPPLSSGPGPOAS 538
DB 692 VTLPISSGGPEGS 704

Query Match 7.9%; Score 233; DB 1; Length 896;
Best Local Similarity 20.4%; Pred. No. 1.3e-08;
Matches 113; Conservative 86; Mismatches 220; Indels 134; Gaps 23;

QY 22 DLVCTDYLQTVICILEMWN-----LHPSTLTLTQDQYEELKDEATSCSLHRS 70
DB 250 NLQCFDGLQSLHCSWEVWTTQTSVGLFVRPSVA-----PEEKCSFVVKPE 299
Q* 71 ANNATHATYCHMDVHFHMADIFSVNITDQSGNYSQEGSFLLA-ESIKAPP-FNVTV 128
DB 300 PGASVYTRYHCSLPPEPSAHSQYTVSVK-----HLEQKFIYSNHIQEPPTLNLT 353
QY 129 TFSQGNYSWSRDYEDPAPYMLKGLQYELQYLRNRPDPAVSPRKLISVDSRSVLLPL 188
DB 354 N-RDSYLSHWETQKWAYSFI-----BHTFQVQYKKSQSDSWEDSKTENLDRAHSMDS 404
QY 189 EPRKDSYELQVRAGPMFGSSYQGTWSEWSDVIFQTSSEELKEGWNPHLLILLVIVF 248
DB 405 QLEPDTSYCARVRKPI--SNYDGIWSKWESEYTKT-DWVPTLWVILLVFLITLL 461
QY 249 IPAFWSLTHPLWRLKWKIWAIVSPERFPMPLYKCGSGDFKKWGAPFTGSSLELGPWSP 308
DB 462 ILRFQGVSYRYRKWKE--KIPNPSKSL-----FQDGGKGLWP--- 499
QY 309 EYPSLEYVYCHPP--RSPAKQLQTELOEPAELVESDGVKPSFWPTAQNSGGSAYSEE 366
DB 500 --PGSMAAFATKPNALQGPQSL-LAEQQ-----GESSYHL 532
QY 367 RDRPYGLVSDIVTVL--DAEGPCTWPCSD--DGYPALDLDAGLEPSPGLDPLLDAG 422
DB 533 EDNVSPLTIEDPIIRVPPSGDTPPAASSESTQLPNVQEGTTPNRPKQLSPD-- 590
QY 423 TTVLSCGCVSAGSPGLGGP-----LGLSLDLRLKPLADGE--DWAGGLPWGRSPG-- 472
DB 591 -----FNGPYLGPQSHSLPDLPLQSGSPQVGGSLKPLPGSLEYMCLAPGQVQ 640
QY 473 -----VSEESAGSPLAGLMDTDFSGFVGSDCSPVECDFTSPGDEGPPRSYLROWVV 525
DB 641 LVPLSQVMGQGMADVQCGSSLETSGSPVEKPNPVELSMEEQEARNDP----- 691
QY 526 IPPPLSSGPGPOAS 538
DB 692 VTLPISSGGPEGS 704

RESULT 5

A45268
interleukin-9 receptor precursor - mouse
C:Species: Mus musculus (house mouse)
C>Date: 27-Jun-1994 #sequence_revision 27-Jun-1994 #text_change 09-Jul-2004

C:Accession: A45268
R:Renauld, J.C.; Druez, C.; Kermouni, A.; Houssiau, F.; Uyttenhove, C.; Van Roost, E.;
Proc. Natl. Acad. Sci. U.S.A. 89, 5690-5694, 1992
A:Title: Expression cloning of the murine and human interleukin 9 receptor cDNAs.
A:Reference number: A45268; MUID:92302307; PMID:1376929
A:Accession: A45268
A:Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-468 <REN>
A:CROSS-references: UNIPROT:Q01114; GB:M84746; NID:gl94044; PIDN:AAA37871.1; PID:g194044
A:Note: authors translated the codon GGG for residue 394 as Glu
C:Keywords: glycoprotein; receptor; T-cell proliferation; transmembrane protein

Query Match 7.5%; Score 221.5; DB 2; Length 468;
Best Local Similarity 23.2%; Pred. No. 3.9e-08;
Matches 134; Conservative 60; Mismatches 181; Indels 203; Gaps 34;

QY 3 RGMAPLALLLLQGGW--CPDLVCTDYLQTVICILEMWNLHPSTLT-----TW--- 51
DB 36 RGVSVP-----EQGGGQKAGACTLSNIIYRIDC-----HWSAPELGQESRAWLLFT 83
QY 52 QDQYEELKDEAT-----SCSLHRSAHNA-----THATYTCMDVHFHMADDFSVNITDQSG 103
DB 84 SNQVTEIKHKCTFWDSCMCTLVLPKEEVFLPFDNFITLHRCI---MGQE--QVSLVD--- 135
QY 104 NYSQEGSFLLAESIKPAPPNV-TVTPSQGNYSWSRDYEDPAPYMLKGLQYELQYLRN 162
DB 136 -----SOYLPRRHILKDPSPDLSQNSVSSRCVLTWGINL---ALEPLITSLSYELAFKR 186
QY 163 RGDPAVSPRKLISVDSRSVLLPLPRKDSYELQVRA-----GPMFGSSYQGTW 214
DB 187 QEEAWEARHKDRIYGV--TWLILEAVELNPGSIYEALRVQMTLESYEDKTEGEYKSHW 244
QY 215 SEWSDPVIFQTSBELKEG-----WNPHELLLLLVIVFIPAFWSLK--THPLWRL-- 263
DB 245 SEWQPVSVF--PSQRRQGLLVPRWQNSASIL-----VVVPIFLTLTGFWHLLFKLSP 295
QY 264 -WKIWI--AVSPERFPMPLYKCGSGDFKKWGAPFTGSSLELGPWSPVSTLEVYSGH 320
DB 296 RLKRIFYQNPSPFAFFHPLYSVYHGDQFQSWTGARRAG----- 333
QY 321 PPRSPAKQLQTELOEPAELVESDGVKPSFWPTAQNSG---GSAYSEERDRPYGLVSI- 376
DB 334 -----POARQNGVSTSSAGSES-----SIW 353
QY 377 DTVTLDAEGPCTWPCSC-----EDDGYPALDLDAGLEPSPGLDPLLDAGTTVLSCGCV 431
DB 354 EAVATLTVSPACPVQFACLKWEATAPGPGI-----PGSEH-----VLPAQGL 396
QY 432 S-AGSPGLGGPLGSLDLRLKPLADGEDWAGGLPWGRSPGVSSEAGSPLAGLMDTDF 490
DB 397 ELEGQPSAYLP-----QEDWA---PLGSARP-PPPDSDSGS----- 428
QY 491 DSGFVGSDCSPVECDFTS-PGDEGPPRSYLROWVVP 527
DB 429 -SDYCMILDCCB--ECHLSAFPGHTESELTLLAQPVALP 463

RESULT 6

A40091
interleukin-3 receptor beta chain precursor - mouse
C:Species: Mus musculus (house mouse)
C>Date: 30-Jun-1993 #sequence_revision 30-Jun-1993 #text_change 09-Jul-2004
C:Accession: A40091; A43022
R:Itoh, N.; Yonehara, S.; Schreurs, J.; Gorman, D.M.; Maruyama, K.; Ishii, A.; Yahara, I.
Science 247, 324-327, 1990
A:Title: Cloning of an interleukin-3 receptor gene: a member of a distinct receptor gene
A:Reference number: A40091; MUID:90117145; PMID:2404337
A:Accession: A40091
A:Status: nucleic acid sequence not shown
A:Molecule type: mRNA
A:Residues: 1-878 <ITO>
A:CROSS-references: UNIPROT:P26954

Exp. Hematol. 19, 973-977, 1991

A;Title: The erythropoietin receptor gene: cloning and identification of multiple transcripts

A;Reference number: A53958; MUID:91372359; PMID:1654273

A;Accession: A53958

A;Molecule type: mRNA

A;Residues: 1-508 <EHR>

R;Penny, L.A.; Forget, B.G.

Genomics 11, 974-980, 1991

A;Title: Genomic organization of the human erythropoietin receptor gene.

A;Reference number: A55280; MUID:92147143; PMID:1664413

A;Accession: A55280

A;Molecule type: DNA

A;Residues: 1-17;381-387;LLEQQQDA'391-395;504-508 <PEN>

A;Note: sequence modified after extraction from NCBI backbone

A;Note: the authors translated the codon GAT for residue 31 as B

A;Note: an insert coming to other published sequences is considered by authors as lik

R;Maouche, L.; Tournamille, C.; Hattab, C.; Boffa, G.; Cartron, J.P.; Chretien, S.

Blood 78, 2557-2563, 1991

A;Title: Cloning of the gene encoding the human erythropoietin receptor.

A;Reference number: I52563; MUID:92399734; PMID:1668607

A;Accession: I52563

A;Status: translated from GB/EMBL/DBDJ

A;Molecule type: DNA

A;Residues: 1-96 <RES>

A;Cross-references: GB:M76595; NID:g182147; PIDN:AAA52393.1; PID:g553281

C;Genetics:

A;Gene: GDB:EPOR

A;Cross-references: GDB:125242; OMIM:133171

A;Map position: 19p13.3-19p13.2

A;Introns: 39/1; 84/2; 143/1; 195/3; 247/1; 276/2; 305/3

C;Superfamily: erythropoietin receptor; cytokine receptor homology

C;Keywords: alternative splicing; cytokine receptor; glycoprotein; transmembrane protein

F;1-24/Domain: signal sequence #status predicted <SIG>

F;25-508/Product: erythropoietin receptor #status predicted <MAT>

F;52-250/Domain: extracellular #status predicted <EXT>

F;52-239/Domain: cytokine receptor homology <CRS>

F;233-237/Region: WSXWS motif

F;251-272/Domain: transmembrane #status predicted <TM>

F;273-508/Domain: intracellular #status predicted <INT>

F;52-62,91-107/Disulfide bonds: #status predicted

F;76/Binding site: carbohydrate (Asn) (covalent) #status predicted

Query Match 7.2%; Score 213; DB 1; Length 508;

Best Local Similarity 21.6%; Pred. No. 1.7e-07;

Matches 127; Conservative 63; Mismatches 175; Indels 224; Gaps 30;

QY 9 LLLLLLQGGWGP-----DILCYTDYLTQVICILE---MWNLHP 44

DB 15 LCLLLAGAAWAPPNLPDPKFSKAALLAARGPEELCTERLEDLVCWEEAASAGVGP 74

QY 45 STLTUTWQDYBELKDEATS-CSLHRSAHNATHATVTHM---DVHFHMADDIFSNIITD 100

DB 75 GNYSPSYQ-----LDEPKLCLRLHQAPARGAVFWSCLPTADTSSFPV---LELRVTA 126

QY 101 QSGNTYSQEGCSFLLAESIKPAPFNVTVF-----SGQYNISWRSD 141

DB 127 ASG-----APYHRVTHINEBWLDPVGLVARLADSGHWLRWLPP 169

QY 142 YEDPAFYMLKGLQYELQYLRNGCDPWASPRKLLSVDSRSVSLPLPERKDDSSVELQVR 201

DB 170 PETP-----MTSHRIYEDVDVSAGNAGSV--ORVILEGRTECVLS-NLRGTRTYTFAVR 221

QY 202 AGFMPGSSYOGYTSWSDSDVIFQTOSELKEGNPHLL--LLLLVIVFIPAFWSLKTHP 259

DB 222 A-RMAEPSGGFWASWSEPVSLTTSFSD-----LDPLILTLILVILVLLTVLLLSHR 275

QY 260 LWRLMKKIW-AVPSPERFMPLYKCGSGDFKKWV---GAPFTGSSLELGPMSPEVPSTL 314

DB 276 R-ALAKQIWPGPSPESEFEGFTTHKGNFQLWLYQNDGCLW-----WSPCTPFTPE 325

QY 315 EYVSHPPRSPAKRIQLTELQPAELVSDGVPKFSFPTAQNSGGSAYSEBRDPYGLV 374

DB 326 D-----PPAS-----LEVLSERC-----WGTMQ----- 343

QY 375 SIDVTITLDAREGCTWPCSCDDGYPAFLDLDAGLEPSPGLDPLLDAGTTVLSCGCVSAG 434
Db ::: ||| | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
344 AVEPGT--DDEGPLLEPVGSEHAQTYIVLVDKWLPR-----SVDIVAMDEGS 401

QY 435 SPCLGGPLGSLDLRLKPPLAGEDWAGGLPWGGRSPGVSESEAGSPFLAGLMDMTDFDSGF 494
Db ::: ||| | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
379 -----NPPSED-----LP-----GPQG-----SVDIVAMDEGS 401

QY 495 VGSDCSPVECDFTSPGOEG-----PPRSYLQWVWP--PP 529
Db :||| | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
402 EASSCSALA---SKPSPEGASAAFEYTILDPSSQLLRPMWLCPELPP 447

RESULT 10
I56563
Interleukin-3 receptor beta-subunit - rat
C:Species: Rattus sp. [rat]
C>Date: 26-Jul-1996 #sequence_revision 26-Jul-1996 #text_change 09-May-2004
C:Accession: I56563
R:Appel, K.; Buttni, M.; Sauter, A.; Gebicke-Haerter, P.J.
J. Neurosci. 15, 5800-5809, 1995
A>Title: Cloning of rat interleukin-3 receptor beta-subunit from cultured microcytes
A:Reference number: I56563; MUID:95370942; PMID:7643220
A:Accession: I56563
A>Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: mRNA
A:Residues: 1-896 <RES>
A:Cross-references: GB:S79263; NID:g1086954; PIDN:AAB35068.1; PID:g1086955
C:Genetics:
A:Gene: rIL-3beta
C:Superfamily: cytokine IL-3/IL-5/GM-CSF receptor common beta chain; cytokine :
C:Keywords: cytokine receptor
F:39-235/Domain: cytokine receptor homology <CRS1>
F:253-433/Domain: cytokine receptor homology <CRS2>

Query Match 7.2%; Score 211.5; DB 2; Length 896;
Best Local Similarity 21.7%; Pred.No. 4.5e-07;
Matches 126; Conservative 79; Mismatches 228; Indels 147; Gaps 28

QY 2 PRGWAAPLLALLQQGWGCP-----DLVCYTDYLTQVICILEMMNLHPSTLTITWQD 53
Db :||| | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
229 PSQWSPEV-----HWDSPTEKDARPQNLOCFDGIQSLNCSEWVTKVTDVSRGLFY 281

QY 54 QYBELKDEATSCLSHRSAINATHAYTCHMDVFHFMAADDIFSVNITDOGNYSQECGSFL 113
Db :||| | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
282 SSSPKAGEKKCPVVKELQASRYTRYHGLSNVDPAAHSQYTSVSK-----RLEGCKFI 335

QY 114 LA-ESIKPAPP-FNTVTFSGGYNTISWSDYEDPAFYMLKGLOYEIQYNRGDPAVASP 171
Db :||| | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
336 ESFNHHIQMPPTTLNLTKN-RDSYSUHWETQKMSPFFI-----QHAFQVYKKKLDRMEDSK 390

QY 172 RRKLISVDSRSVLLPLEPRKDDSYELOVRAGPFGSGSYOGTWSWSDPDVIFQTSEEK 231
Db :||| | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
391 TENLNHAHND--LP-QLEPCTSICARVRKTIP-EYKGLSWSEMSNECTWTTD---- 439

QY 232 EGW-NPHL---LLLLLVTVFTA--FWSLKTHPLRWLWKKIWAVPSPERFPWPLYKGS 285
Db :||| | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
440 --VMWPTLVILVLIPLIITLLALRFNGCIYCKLYRRWKEKINPNKSLLFDQGGKGL- 496

QY 286 GDFKWVGAPFTGSSLGLGPWSPVSTLEVYSCHP-PRSPAKRLQLTELQEPAELVESD 344
Db :||| | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
497 -----WPP--GSTVTFSSKNPTPGQPNNL-FSELQ----- 524

QY 345 GVPKPSFWPTAQNSGGSAYSEBRDRPYGLVISDTITVL--DAEGFCTWPCSCDDGYPAL 402
Db :||| | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
525 -----GVSYTHLEDNVSPLETIEDPNIIRDSPSGDPTTPAASSEP----- 564

QY 403 DLDAGLEPSPGLE-DPLLDAGTTVLSCGCVSAGSPGLCGPI-----GSLD-----R 448
Db :||| | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
565 -----MEQSNNVOVDPTILSGRPKRQLPSFDPNGNYLGPPOSHSLPDLPGQLVSPQGVGS 619

QY 449 LKPLADGEDWAGGLPWGGRSPGVSEAGSPFLAGLMDMTDFDSGFVGS 498
Db :||| | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
498 -----VSESEAGSPFLAGLMDMTDFDSGFVGS 498

Db	620	LKPAL-----PGSLRYMCLPPGQVOLVPLSQVMGQGRDQVQCGSSLETTSPSMESR	673
Qy	499	CSSPVEECDFTSPDEGPPRSYLRQWVVIPIPLSSPGQAS	538
Db	674	ESPVEL-----KEEQEPDN-----PVTLPISSGPKDS	704
RESULT 11			
A39255			
Cytokine receptor common beta chain precursor - human			
C:Species: Homo sapiens (man)			
C:Date: 30-Jun-1993 #sequence_revision 30-Jun-1993 #text_change 09-May-2004			
C:Accession: A39255			
R:Hayashida, K.; Kitamura, T.; Gorman, D.M.; Arai, K.; Yokota, T.; Miyajima, A.			
Proc. Natl. Acad. Sci. U.S.A. 87, 9655-9659, 1990			
A:Title: Molecular cloning of a second subunit of the receptor for human granulocyte-macrophage colony-stimulating factor			
A:Reference number: A39255; MUID:91088571; PMID:1702217			
A:Accession: A39255			
A:Molecule type: mRNA			
A:Residues: 1-897 <HAY>			
A:Cross-references: GB:M38275			
C:Comment: The human high-affinity IL-3, IL-5, and GM-CSF receptors have ligand-specificity			
C:Genetics:			
A:Gene: GDB:CSF2RB			
A:Cross-references: GDB:126838; OMIM:138981			
A:Map position: 22q13.1-22q13.1			
C:Superfamily: cytokine IL-3/IL-5/GM-CSF receptor common beta chain; cytokine receptor h			
C:Keywords: alternative splicing; cytokine receptor; duplication; transmembrane protein			
F:1-16/Domain: signal sequence #status predicted <SIG>			
F:17-897/Product: cytokine receptor common beta chain #status predicted <MAT>			
F:17-443/Domain: extracellular #status predicted <EXT>			
F:35-232/Domain: cytokine receptor homology <CRS1>			
F:250-431/Domain: cytokine receptor homology <CRS2>			
F:444-460/Domain: transmembrane #status predicted <TM>			
F:461-897/Domain: intracellular #status predicted <INT>			
Query Match 6.9%; Score 204; DB 1; Length 897;			
Best Local Similarity 22.6%; Pred. No. 1.5e-06;			
Matches 142; Conservative 66; Mismatches 219; Indels 200; Gaps 32;			
Qy	22	DLVCYTDYLTQVLCILEMNNLHPSTLT--LTWQDQVEELKDEATSC-----SLHRSAH-	72
Db	247	NLECFDGAAVLSCSWEVKREKVASVFGLPSPDAGEECSVLREGLSLHTRHHC	306
Qy	73	-----NATHATYTCMDVDFHFMADDFISVNIITDQSGNYSQEGCSFLLAESIKPAPFNV	126
Db	307	QIPVPDPATHQY-----IVSV---QPRAEKHKS---SVNIQWAPP-SL	345
Qy	127	TVTFSG-QYNNISW-----RSYEDDPAYMLKGLQYELQYLRNGDPWAVSPKRLTSVDS	180
Db	346	NVTXGDSYSLRWETMKRYEHIDHTF-----EIQYRKDTATWKDSKTETL--QNA	394
Qy	181	RSVSLLLPLEFKOSSYELQVRAGMPGSSYQGTWSESDPVIQTQSEELKEGNWPHLL	240
Db	395	HSMALPALE--PSTRYWARVRV-RTSTGTNGIINSEARSWDTES--VLPWV-----	443
Qy	241	LLILVIVFIPA-----FWSLKTPLWRLWKIKIIVAPSPERFFMPLYKCGSGDFKKN--	291
Db	444	VLALIVFLITAVLLALRFGCIQYRLRRKWEKIPNPSKSHLFQ-----NGSAELWPP	497
Qy	292	--VGAPPTGSLLEIGPWS---PEV-----PSTLE--VYSCHPPSPAKRLQ	330
Db	498	GSMSAFTSGSPHQPGWGRFRPELEGVFPFGDGEVSPSLTIEDPKHVCDDPPSGFDPTTPA	57
Qy	331	LTELQEAELVESDVPKPSFWPMTAQNSSGGSAYSEERDRPVGLVSDITVTLDAEGPCTW	390
Db	558	ASDLPTTQPPSPQGPAAASHTPKQASS-----FDENGPIYG	595
Qy	391	P---CSCEDD--GYPALDLDALESP---GLEPDLLDAGTTLVSCGCVSAGSPGLG----	439
Db	596	PPHSRSLPDIIGQPPPEQEGSGOKSPPPGSLVYLCLPAGGOVOLVPLQAQMGPCQAVEVE	655

QY 440 -----GPIGSLDLRLKPPADGEDWAGGLPWGGRSP-----GGVSESEAGSPLAGLDM 487
Db 656 RPSQGAAGS-----PSLESG-----GGPAPPALGPRVGGQDKDSVPAIPMSG 700
QY 488 DTFSGFVSGDCSSPVECDFT-----SPGDEGPP 516
Db 701 DTEDPG-VASGVYSSADLVFTNSGASSVSLVPSLGLPSDQFPLCPGLASGPPGAPGV 759
QY 517 RYLQWVVVIPP-----PLSSQGP 535
Db 760 KSGFEGYVELPPIEGRSPPRNVPV 786

RESULT 12
A32385
erythropoietin receptor precursor, membrane-bound form - mouse
C:Species: Mus musculus (house mouse)
C:Date: 28-Sep-1990 #sequence revision 05-Apr-1995 #text_change 09-Jul-2004
C:Accession: A41686; S13249
R:Hino, M.; Tojo, A.; Misawa, Y.; Morii, H.; Takaku, F.; Shibuya, M.
Mol. Cell. Biol. 11, 5527-5533, 1991
A:Title: Unregulated expression of the erythropoietin receptor gene caused by insertion
A:Reference number: A41686; MUID:92017832; PMID:1656233
A:Accession: A41686
A:Molecule type: mRNA
A:Residues: 1-507 <HIN>
A:Cross-references: UNIPROT:PI4753; GB:S59388; NID:G237036; PIDN:AAB20029.1; PID:G237037
A:Experimental source: murine erythroleukemia (MEL) cell line F5-5
R:D'Andrea, A.D.; Lodish, H.F.; Wong, G.G.
Cell 57, 277-285, 1989
A:Title: Expression cloning of the murine erythropoietin receptor.
A:Reference number: A32385; MUID:89195238; PMID:2539263
A:Accession: A32385
A:Molecule type: mRNA
A:Residues: 1-507 <DAA>
A:Cross-references: GB:J04843; NID:G193090; PIDN:AAA37571.1; PID:G309219
A:Experimental source: murine erythroleukemia (MEL) cells, subclone 745
J. Mol. Biol. 216, 567-575, 1990
R:Kuramochi, S.; Ikawa, Y.; Todokoro, K.
A:Title: Characterization of murine erythropoietin receptor genes.
A:Reference number: S13249; MUID:91080149; PMID:2175360
A:Accession: S13249
A:Molecule type: DNA; mRNA
A:Residues: 1-507 <URS>
A:Cross-references: EMBL:X53081; NID:G50861; PIDN:CAA37248.1; PID:G50862
A:Experimental source: murine erythroleukemia K-1 cells
C:Genetics:
A:Introns: 39/1; 83/2; 142/1; 194/3; 246/1; 275/2; 304/3
C:Superfamily: erythropoietin receptor; cytokine receptor homology
F:1-24/Domain: alternative splicing; cytokine receptor; glycoprotein; transmembrane protein
F:1-24/Domain: signal sequence #status predicted <SIG>
F:25-507/Product: erythropoietin receptor #status predicted <EXT>
F:25-507/Product: extracellular #status predicted <EXT>
F:52-238/Domain: cytokine receptor homology <CRS>
F:250-271/Domain: transmembrane #status predicted <TMM>
F:272-507/Domain: intracellular #status predicted <INT>
F:75/Binding site: carbonyl bonds: #status predicted
F:75/Binding site: carbonyl bonds: (Asn) (covalent) #status predicted

Query Match 6.8%; Score 201; DB 1; Length 507;
Best Local Similarity 23.1%; Pred. No. 1.2e-06;
Matches 117; Conservative 60; Mismatches 188; Indels 142; Gaps 27;
QY 2 PRGWAAPLILLLLQGGW-----GCPDLVCYTDYLTQVICILEMW 40
Db 10 PR--VGPCLLLLAGA WAPSLSLPDPKESKAALLASRGSELLCTQRLDVLVCFWE-- 65
QY 41 NLHPTLTLTWQDQVEELKDEATSCSLHRSAAHNAHTATYTCM----DVHFHMADDIFSVN 97
Db 66 EAASGMDFNYSFVSQLEGESEKSKSLHQAFTVRGSRVFWCSLPTADTSSFPV---LELQ 122
QY 98 ITDQGN--YSQ-----ECGSFLLAES-----IKPAPPFNVTTFSCQYNIS 137

QY 440 -----GPIGSLDLRLKPPADGEDWAGGLPWGGRSP-----GGVSESEAGSPLAGLDM 487
Db 656 RPSQGAAGS-----PSLESG-----GGPAPPALGPRVGGQDKDSVPAIPMSG 700
QY 488 DTFSGFVSGDCSSPVECDFT-----SPGDEGPP 516
Db 701 DTEDPG-VASGVYSSADLVFTNSGASSVSLVPSLGLPSDQFPLCPGLASGPPGAPGV 759
QY 517 RYLQWVVVIPP-----PLSSQGP 535
Db 760 KSGFEGYVELPPIEGRSPPRNVPV 786

RESULT 12
A32385
erythropoietin receptor precursor, membrane-bound form - mouse
C:Species: Mus musculus (house mouse)
C:Date: 28-Sep-1990 #sequence revision 05-Apr-1995 #text_change 09-Jul-2004
C:Accession: A41686; S13249
R:Hino, M.; Tojo, A.; Misawa, Y.; Morii, H.; Takaku, F.; Shibuya, M.
Mol. Cell. Biol. 11, 5527-5533, 1991
A:Title: Unregulated expression of the erythropoietin receptor gene caused by insertion
A:Reference number: A41686; MUID:92017832; PMID:1656233
A:Accession: A41686
A:Molecule type: mRNA
A:Residues: 1-507 <HIN>
A:Cross-references: UNIPROT:PI4753; GB:S59388; NID:G237036; PIDN:AAB20029.1; PID:G237037
A:Experimental source: murine erythroleukemia (MEL) cell line F5-5
R:D'Andrea, A.D.; Lodish, H.F.; Wong, G.G.
Cell 57, 277-285, 1989
A:Title: Expression cloning of the murine erythropoietin receptor.
A:Reference number: A32385; MUID:89195238; PMID:2539263
A:Accession: A32385
A:Molecule type: mRNA
A:Residues: 1-507 <DAA>
A:Cross-references: GB:J04843; NID:G193090; PIDN:AAA37571.1; PID:G309219
A:Experimental source: murine erythroleukemia (MEL) cells, subclone 745
J. Mol. Biol. 216, 567-575, 1990
R:Kuramochi, S.; Ikawa, Y.; Todokoro, K.
A:Title: Characterization of murine erythropoietin receptor genes.
A:Reference number: S13249; MUID:91080149; PMID:2175360
A:Accession: S13249
A:Molecule type: DNA; mRNA
A:Residues: 1-507 <URS>
A:Cross-references: EMBL:X53081; NID:G50861; PIDN:CAA37248.1; PID:G50862
A:Experimental source: murine erythroleukemia K-1 cells
C:Genetics:
A:Introns: 39/1; 83/2; 142/1; 194/3; 246/1; 275/2; 304/3
C:Superfamily: erythropoietin receptor; cytokine receptor homology
F:1-24/Domain: alternative splicing; cytokine receptor; glycoprotein; transmembrane protein
F:1-24/Domain: signal sequence #status predicted <SIG>
F:25-507/Product: erythropoietin receptor #status predicted <EXT>
F:25-507/Product: extracellular #status predicted <EXT>
F:52-238/Domain: cytokine receptor homology <CRS>
F:250-271/Domain: transmembrane #status predicted <TMM>
F:272-507/Domain: intracellular #status predicted <INT>
F:75/Binding site: carbonyl bonds: #status predicted
F:75/Binding site: carbonyl bonds: (Asn) (covalent) #status predicted

Query Match 6.8%; Score 201; DB 1; Length 507;
Best Local Similarity 23.1%; Pred. No. 1.2e-06;
Matches 117; Conservative 60; Mismatches 188; Indels 142; Gaps 27;
QY 2 PRGWAAPLILLLLQGGW-----GCPDLVCYTDYLTQVICILEMW 40
Db 10 PR--VGPCLLLLAGA WAPSLSLPDPKESKAALLASRGSELLCTQRLDVLVCFWE-- 65
QY 41 NLHPTLTLTWQDQVEELKDEATSCSLHRSAAHNAHTATYTCM----DVHFHMADDIFSVN 97
Db 66 EAASGMDFNYSFVSQLEGESEKSKSLHQAFTVRGSRVFWCSLPTADTSSFPV---LELQ 122
QY 98 ITDQGN--YSQ-----ECGSFLLAES-----IKPAPPFNVTTFSCQYNIS 137

Db 123 VTEASGSPRYHRIIHIINEWVLLDAPAGLLARRAEBGSHVLRWLWLPFGAPMTTHIRYEV- 181
QY 138 WRSDYEDPAFYMLKGLQYELQYRNRPDPWAPRPRKLIISVDSRSVSLPLPLEFRKDSYVE 197
Db 182 -----DVSAGNR-----AGGTQREVLEGRTECVLS-NLRGGTRYT 216
QY 198 LQVRAGPMPGSSYQGTWSESDPVIQTQSEBELKGNWPHLLLLLLLVIVFIP---AFWS 254
Db 217 FAVRA-RMAEPFSGFWSAMSEPALLTASD-----LDP-LILTULSLVLISLLLTUVA 269
QY 255 LKTHPLWRLWKIIV-APVSPRFRFMPLYKGGSGDFKKWV---GAPFTGSSLELGPWSPE 309
Db 270 LLSHR- TLQKIWPGISPESEPEGLFTTHKGNFQLMLQRLQDGLW-----WSPG 319
QY 310 VPSTLEVYVCHPPRSPAKRLQITELQEPALVESDVP-----KPSFWPTAQNNGSGAY- 363
Db 320 -----SSFPEDPPA---HLEVLSEPRWAVTQAGDPGADDEGPLEPVGSEHAQDTYL 368
QY 364 -----SEERDRPYGLVSTDTVTVLDAAEGPCTWPCSCEDDGYVPALDLDAGLEPS 411
Db 369 VLDKMLLPRTPCSENLSPGG--SVDPVTMDSEATSSCPDLSLASKPRP-----EGTSFS 421
QY 412 PGLDPLLDAGTTVLSCCVCVSGAGSPGL 438
Db 422 -SFEVTILDPSQLL---CPRALPPEL 444

RESULT 13
A46713
erythropoietin receptor precursor - rat
C:Species: Rattus norvegicus (Norway rat)
C:Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 09-Jul-2004
R:Masuda, S.; Nagao, M.; Takahata, K.; Konishi, Y.; Gallyas Jr., F.; Tabira, T.; Sasaki, J. Biol. Chem. 268, 11208-11216, 1993
A:Title: Functional erythropoietin receptor of the cells with neural characteristics. C
A:Reference number: A46713; MUID:93266574; PMID:7684373
A:Accession: A46713
A:Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-507 <MAS>
A:Cross-references: UNIPROT:Q07303; GB:D13566; NID:G286209; PIDN:BAA02761.1; PID:G286210
A:Experimental source: PC12 and erythroid cells
A:Note: sequence extracted from NCBI backbone (NCBIN:132811, NCBIP:132813)
C:Superfamily: erythropoietin receptor; cytokine receptor homology
C:Keywords: cytokine receptor; glycoprotein; transmembrane protein
F:1-24/Domain: signal sequence #status predicted <SIG>
F:25-507/Product: erythropoietin receptor #status predicted <MAT>
F:25-249/Domain: extracellular #status predicted <EXT>
F:52-238/Domain: cytokine receptor homology <CRS>
F:250-271/Domain: transmembrane #status predicted <TMM>
F:272-507/Domain: intracellular #status predicted <INT>
F:75/Binding site: carbonyl bonds: (Asn) (covalent) #status predicted

Query Match 6.6%; Score 195; DB 1; Length 507;
Best Local Similarity 21.4%; Pred. No. 3.2e-06;
Matches 126; Conservative 70; Mismatches 194; Indels 198; Gaps 32;
QY 2 PRGWAAPLILLLLQGGW-----GCPDLVCYTDYLTQVICILEMW 40
Db 10 PR--VSPCLLLLAGA WASSPSLPDPKESKAALLASRGSELLCTQRLDVLVCFWE-- 65
QY 41 NLHPTLTLTWQDQVEELKDEATSCSLHRSAAHNAHTATYTCM----DVHFHMADDIFSVN 97
Db 66 EAASGMDFNYSFVSQLEGESEKSKRLHQAFTVRGSRVFWCSLPTADTSSFPV---LELQ 122
QY 98 ITDQGN--YSQ-----ECGSFLLAES-----IKPAPPFNVTTFSCQYNIS 137
Db 123 VTEASGSPRYHRIIHIINEWVLLDAPAGLLARRAEBGSHVLRWLWLPFGAPMTTHIRYEV- 181
QY 138 WRSDYEDPAFYMLKGLQYELQYRNRPDPWAPRPRKLIISVDSRSVSLPLPLEFRKDSYVE 197
Db 182 -----DVSAGNR-----AGGTQREVLEGRTECVLS-NLRGGTRYT 216

acellular domain and may encode a soluble form of the receptor
R:Harada, N.; Castle, B.E.; Gorman, D.M.; Itoh, N.; Schreurs, J.; Barrett, R.L.; Howard,
Proc. Natl. Acad. Sci. U.S.A. 87, 857-861, 1990
A:Title: Expression cloning of a cDNA encoding the murine interleukin 4 receptor based o
A:Reference number: A34861; MUID:90138976; PMID:2405398
A:Accession: A34861
A:Molecule type: mRNA
A:Residues: 1-810 <HAR>
A:Cross-references: GB:M29854; NID:gl98346; PIDN:AAA39297.1; PID:g309407
R:Wrighton, N.C.; Campbell, L.A.; Lee, F.D.
Growth Factors 6, 103-118, 1992
A:Title: The murine interleukin-4 receptor gene: Genomic structure, expression and pote
A:Reference number: I54232; MUID:92265335; PMID:1534014
A:Accession: I54232
A>Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 1-73, '1', '75-333', 'P', '335-810' <RES>
A:Cross-references: GB:M64879; NID:gl98359; PIDN:AAB59727.1; PID:g198361
C:Genetics:
A:Introns: 24/1; 71/2; 122/1; 172/3; 225/1; 258/2; 284/3; 301/2
C:Superfamily: interleukin-4 receptor; cytokine receptor homology
C:Keywords: alternative splicing; cytokine receptor; glycoprotein; transmembrane protein
F:1-25/Domain: signal sequence #status predicted <SIG>
F:26-810/Product: interleukin-4 receptor #status experimental <MAT>
F:26-233/Domain: extracellular #status predicted <EXT>
F:34-219/Domain: cytokine receptor homology <CRS>
F:234-257/Domain: transmembrane #status predicted <TM>
F:258-810/Domain: intracellular #status predicted <INT>
F:72,129,135,163,177/Binding site: carbohydrate (Asn) (covalent) #status predicted

Query Match 6.4%; Score 189.5; DB 1; Length 810;
-Best Local Similarity 20.9%; Pred. No. 1.4e-05;
Matches 159; Conservative 70; Mismatches 222; Indels 309; Gaps 42;
QY 9 LLLLLLGGGCGPDL---VCYTDYLTQVICILEMNLH-----PSTLTITLTDQOYEELKD 60
D8 15 LLLLLVTGSGSKVLGEPTCFSDYRTSTC---EWFLDASVDCSSQCLHYELMFPFSE 71
QY 61 EATSCSLHRSAINATHATYTCMDVPHFMADDIFSVNIITDQSGNYSQEC-----GS 111
D8 72 NLTCI-----PRNSASTVCVCHE-----MNRPVQSDRYQMELWAEHRQLWQGS 115
QY 112 FLAASIKPAPFNTV--TFSGQYNISWRDY-----EDPAFYML 150
D8 116 FSPGNVPLADNLTHTNVSDWLLTWNLYPNLNLYKDLISWNIISREDNPAEFIV 175
QY 151 KGLQYELQYNRGDPWAVSPRRKLISVDSRSVLLPLEFRKDSYVELQVRAGMPGSSY 210
D8 176 -----YNYTK---EPRLSFPINILMS-----GVYTYARV---VRSQIL 209
QY 211 QCTWSESDPVITFQTSBELKEGWNPHLLLLL-----LVIVFIPAPMSLKTHTPLWR 262
D8 210 TGTWSEWSPSIT-----WYNHFQPLIQRPLGLVTISCLICPLFCYFSITK 258
QY 263 LWKKIW--AVSPPERFFM-----PLYKGC----- 284
D8 259 I-KKIWDQIPTAPSPVAIIIQDAQVPLMDKQTSQESTKYPHWKTCLDKLPLCLKH 317
QY 285 ----SGDFKKWGPAPFTGSSLEGP--WSP-EVPSTLEVYSCHPPSPAKRLQLTELOB- 336
D8 318 RVKKTDPFK--AAP-TKSLQSPGKAGCMEVSRIV-----LWPNVSVSVVRCMELFEA 370
QY 337 PAELV--ESDGVKPSFWNPTAQNSSGAYSE-ERDRPYGLNSIDTIVTLDAE----- 385
D8 371 PVQNVEEDEIVKEDLSMSPNSGCGFQESQADIMARLTENLFSDLLEAENGGLQSA 430
QY 386 -----GPCTWPC-----SCDDGYPALDLIDAGLEFSPGLEDPILLDAG 422
D8 431 LAESCSPLPSGSGQASVSWACLPMGPSEATCQVTEQPS-----HFCPLSGSPAQAP 483
QY 423 TTVLSCG-----CVSAGSPGLGGLGSLDLRLK----- 450
D8 484 T--LACTQVPLVADNPATYRFSDCSPAPNPGELAPESQOQQADHLEEEEPSPADPHSSG 541

QY 451 PPLADGEDW-----AGG--LPWGG-----RSPGGVSESEAGSP 481
D8 542 PPMQPVESWEQILHMSVLQHGAAAGSTPAPAGGYQEFVQAVKQGAQDQGVGVPSGDP 601
QY 482 -----LAGLMDMT-----FDSGFVG-----SDCSSPVECDFT----- 508
D8 602 GYKAFSSLLSSNGIRGDTAAAGTDDHGCGYKPFQNPVNPQSPSSVPL-----FTFGLDTELS 658
QY 509 -SPGDEGPPRSYLR-----QWVVIPLPLSS-RGP 535
D8 659 PSPLNSDPKSPPECLGLELGLKGGDWKARPPADQVPKP 698

Search completed: July 9, 2005, 11:47:52
Job time : 46 secs

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GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: July 9, 2005, 11:28:19 ; Search time 161 Seconds
(without alignments)
1292.404 Million cell updates/sec

Title: US-10-620-169-4

Perfect score: 2958

Sequence: 1 MPRGWAPLILLLLQGWC.....YLQWVIPPPLSPGPQAS 538

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 2105692 seqs, 386760381 residues

Total number of hits satisfying chosen parameters: 2105692

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : A_Geneseq_16Dec04.*

1: Genesep1980s.*

2: Genesep1990s.*

3: Genesep2000s.*

4: Genesep2001s.*

5: Genesep2002s.*

6: Genesep2003as.*

7: Genesep2003bs.*

8: Genesep2004s.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	2958	100.0	538	2 AAY27450	Human MU-
2	2958	100.0	538	3 AAB18634	A human z
3	2958	100.0	538	3 AAY45031	HUMAN Orp
4	2958	100.0	538	3 AAY69886	Human hae
5	2958	100.0	538	3 AAY79312	Human cyt
6	2958	100.0	538	4 AAB48001	Human IL-
7	2958	100.0	538	5 ABB81960	Human 164
8	2958	100.0	538	5 AAU11912	Human MU-
9	2958	100.0	538	5 AAE13726	Human sol
10	2958	100.0	538	5 AAU11978	Human zal
11	2958	100.0	538	6 ABE1402	Human IL-
12	2958	100.0	538	7 ABE14939	Human int
13	2958	100.0	538	7 ABE14939	Human MU-
14	2958	100.0	538	7 ABW00881	Human cyt
15	2958	100.0	538	7 ADG87460	Human zal
16	2958	100.0	538	7 ADH44685	Human zal
17	2958	100.0	538	7 ADI10121	Immunity-
18	2958	100.0	538	8 ADH10505	Human int
19	2958	100.0	538	8 ADJ25623	Human int
20	2958	100.0	538	8 ADM83456	Human PRO
21	2958	100.0	538	8 ADI91861	Human zal
22	2958	100.0	538	8 ADP19844	Human zal
23	2958	100.0	538	8 ADS82585	Interleuk
24	2951	99.8	538	3 AAY94304	Human HNO
25	2951	99.8	538	4 AAU08728	Human HNO

26	2933	99.2	538	4 AAE02459	Human DNA
27	2905	98.2	538	3 AAY69888	Mouse hae
28	2817	95.2	568	3 AAY94305	Human HNO
29	2817	95.2	568	4 AAE02457	Human DNA
30	2817	95.2	568	4 AAU08729	Human HNO
31	2817	95.2	568	5 AAE13738	Human sol
32	1899.5	64.2	361	3 AAY69883	Human hae
33	1735.5	58.7	529	3 AAY79320	Mouse cyt
34	1735.5	58.7	529	5 AAU11915	Mouse MU-
35	1735.5	58.7	529	5 AAE13730	Mouse sol
36	1735.5	58.7	529	6 ABR61405	Murine IL
37	1735.5	58.7	529	7 ABU62891	Mouse MU-
38	1735.5	58.7	529	7 ABW00888	Mouse zal
39	1735.5	58.7	529	7 ADG87543	Mouse zal
40	1735.5	58.7	529	8 ADM83539	Mouse zal
41	1735.5	58.7	529	8 ADS82587	Interleuk
42	1729.5	58.5	529	4 AAB48002	Murine IL
43	1729.5	58.5	529	5 ABB81961	Mouse 164
44	1729.5	58.5	529	5 AAE24986	Mouse OCR
45	1729.5	58.5	529	5 ABB33048	Mouse OCR

ALIGNMENTS

RESULT 1

AAAY27450

ID AAY27450 standard; protein; 538 AA.

AC AAY27450;

DT 26-NOV-1999 (first entry)

DE Human MU-1 hematopoietin receptor protein.

KW MU-1 hematopoietin receptor protein; e MU-1 protein; gene therapy;

KW cell proliferation; cytokine production; immune response; cancer;

KW autoimmune disease; transplant rejection; hematopoiesis; anemia;

KW gene mapping; nutritional supplement; human.

OS Homo sapiens.

PN WO9947675-A1.

PD 23-SEP-1999.

PF 17-MAR-1999; 99WO-US005854.

PR 17-MAR-1998; 98US-00040005.

PA (GENY) GENETICS INST INC.

PI Donaldson D, Ungar M;

XX WPI; 1999-562115/47.

XX N-PSDB; AAZ07535.

XX New nucleic acid encoding the MU-1 hematopoietin receptor protein, used

for treating e.g. cancer, autoimmune disease or abnormal hematopoiesis.

XX Claim 9; Page 33-35; 37pp; English.

XX This represents a MU-1 hematopoietin receptor protein. The protein can be produced by standard recombinant methodology. The MU-1 protein has the biological activity of the MU-1 hematopoietin receptor superfamily chain. It is used to screen for specific binding agents; to raise specific antibodies; as assay reagents, tissue markers etc. and therapeutically (optionally expressed from the MU-1 gene by gene therapy). Many possible activities/uses of the MU-1 protein are described without supporting evidence, e.g. they regulate cell proliferation and differentiation, induce production of cytokines, stimulate or suppress an immune response (e.g. for treating immune deficiency of any etiology, cancer or autoimmune disease, and for preventing transplant rejection) and regulate

CC of hematopoiesis, e.g. for treating anemia. The MU-1 gene is used as a
CC research reagent, for recombinant production of the protein, as tissue or
CC molecular weight marker, for gene mapping; for production of anti-DNA or
CC anti-protein antibodies etc. the MU-1 protein and the nucleic acids are
CC also useful as nutritional supplements or sources and the antibodies can
CC be used therapeutically, as assay reagents and for affinity purification
XX
XX
SQ Sequence 538 AA;

Query Match 100.0%; Score 2958; DB 2; Length 538;
Best Local Similarity 100.0%; Pred. No. 6.2e-240;
Matches 538; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MPRGWAAPLLLLLGGGCPDLVCYDYLTQVICILEMNNLHPSTLTLTWQDOVEELKD 60
DB 1 MPRGWAAPLLLLLGGGCPDLVCYDYLTQVICILEMNNLHPSTLTLTWQDOVEELKD 60
QY 61 EATCSLHRSAHNATHATYTCCHMDVHFHMADDIFSVNITDQSGNYSCQSGFLLAESIKP 120
DB 61 EATCSLHRSAHNATHATYTCCHMDVHFHMADDIFSVNITDQSGNYSCQSGFLLAESIKP 120
QY 121 APPFNVTTFSGQYNIWSRSDYEDPAFYLKGLQYELQYRNRPWAVSPRKLISYDS 180
DB 121 APPFNVTTFSGQYNIWSRSDYEDPAFYLKGLQYELQYRNRPWAVSPRKLISYDS 180
QY 181 RSVSLLPLEFRKDSYELQVRAGMPGSSYQGTWSESDPVIQTQSEELKEGWNPHLLL 240
DB 181 RSVSLLPLEFRKDSYELQVRAGMPGSSYQGTWSESDPVIQTQSEELKEGWNPHLLL 240
QY 241 LLLLVIIVFIPAFWSLTKTHPLWRLWKKIWAVSPERFFMPLYKGCSDGDFKWWGAPFTGSS 300
DB 241 LLLLVIIVFIPAFWSLTKTHPLWRLWKKIWAVSPERFFMPLYKGCSDGDFKWWGAPFTGSS 300
QY 301 LELGWPSEVPSTLTVYSCHPSPRPAKRLQLTQELQEPALVESDGVKPSFWPTAQNCGG 360
DB 301 LELGWPSEVPSTLTVYSCHPSPRPAKRLQLTQELQEPALVESDGVKPSFWPTAQNCGG 360
QY 361 SAYSEERDRPYGLVSDITVTVLDAEGPCTWPCSCDDGYPALDLDAGLEPSPGLEDPDLD 420
DB 361 SAYSEERDRPYGLVSDITVTVLDAEGPCTWPCSCDDGYPALDLDAGLEPSPGLEDPDLD 420
QY 421 AGTTVLSGCVSAGSPGLGGPLGSLDLRLKPLADGEDWAGGLPWGGRSPGVSESEAGS 480
DB 421 AGTTVLSGCVSAGSPGLGGPLGSLDLRLKPLADGEDWAGGLPWGGRSPGVSESEAGS 480
QY 481 PLAGLDMDTFDSGFGVSDCSSPVECDFTSPGDEGPPRSYLQWVVIPIPLSSPGQAS 538
DB 481 PLAGLDMDTFDSGFGVSDCSSPVECDFTSPGDEGPPRSYLQWVVIPIPLSSPGQAS 538

RESULT 2

AAB18634

ID AAB18634 standard; protein; 538 AA.

XX

AC AAB18634;

XX

DT 22-JAN-2001 (first entry)

XX

DE A human zalphall ligand polypeptide.

XX

KW zalphall ligand; cytokine; haematopoietic cell proliferation; lymphoma;

KW tumorigenesis; leukaemia; hematopoiesis; B cell tumour.

XX

OS Homo sapiens.

XX

PN WO200053761-A2.

XX

PD 14-SEP-2000.

XX

PF 09-MAR-2000; 2000WO-US006067.

XX

PR 09-MAR-1999; 99US-00264908.

PR 11-MAR-1999; 99US-00265992.

PR 01-JUL-1999; 99US-0142013P.

XX (ZYMO) ZYMOGENETICS INC.

PA

XX Novak JE, Presnell SR, Sprecher CA, Poster DC, Holly RD;

PI Gross JA, Johnston JV, Nelson AJ, Dillon SR, Hammond AK;

XX

DR WPI; 2000-565600/52.

XX N-PSDB; RAA75557.

DR

XX New human cytokine, designated zalphall ligand, useful for stimulating

PT the proliferation and/or development of hematopoietic cells in vitro and

PT in vivo, and for treating tumorigenesis.

XX

XX Disclosure; Page 255-256; 256pp; English.

XX

CC The present sequence represents a human zalphall ligand polypeptide,

CC which is a cytokine. The zalphall ligand is useful for stimulating the

CC proliferation and development of haematopoietic cells in vitro and in

CC vivo. Zalphall ligand polynucleotides can be used as primers or probes

CC for cloning the zalphall gene. The zalphall ligand is useful for treating

CC tumorigenesis. A zalphall ligand-saporin fusion toxin may be used for

CC treating leukaemias and lymphomas. Antagonists against zalphall ligand

CC are useful as research reagents for characterizing ligand-receptor

CC interaction. Antagonists are also useful for inhibiting expansion,

CC proliferation, activation and differentiation of cells involved in

CC regulating hematopoiesis. The zalphall ligand may also be used to

CC stimulate an immune response against B cell tumour, a virus, a parasite

CC or a bacterium. The zalphall polypeptides, polynucleotides, antagonists,

CC agonists and antibodies are also useful for the detection, diagnosis,

CC prevention, and treatment of diseases associated with a zalphall ligand

CC genetic defect

XX

SQ Sequence 538 AA;

Query Match 100.0%; Score 2958; DB 3; Length 538;

Best Local Similarity 100.0%; Pred. No. 6.2e-240;

Matches 538; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MPRGWAAPLLLLLGGGCPDLVCYDYLTQVICILEMNNLHPSTLTLTWQDOVEELKD 60
DB 1 MPRGWAAPLLLLLGGGCPDLVCYDYLTQVICILEMNNLHPSTLTLTWQDOVEELKD 60
QY 61 EATCSLHRSAHNATHATYTCCHMDVHFHMADDIFSVNITDQSGNYSCQSGFLLAESIKP 120
DB 61 EATCSLHRSAHNATHATYTCCHMDVHFHMADDIFSVNITDQSGNYSCQSGFLLAESIKP 120
QY 121 APPFNVTTFSGQYNIWSRSDYEDPAFYLKGLQYELQYRNRPWAVSPRKLISYDS 180
DB 121 APPFNVTTFSGQYNIWSRSDYEDPAFYLKGLQYELQYRNRPWAVSPRKLISYDS 180
QY 181 RSVSLLPLEFRKDSYELQVRAGMPGSSYQGTWSESDPVIQTQSEELKEGWNPHLLL 240
DB 181 RSVSLLPLEFRKDSYELQVRAGMPGSSYQGTWSESDPVIQTQSEELKEGWNPHLLL 240
QY 241 LLLLVIIVFIPAFWSLTKTHPLWRLWKKIWAVSPERFFMPLYKGCSDGDFKWWGAPFTGSS 300
DB 241 LLLLVIIVFIPAFWSLTKTHPLWRLWKKIWAVSPERFFMPLYKGCSDGDFKWWGAPFTGSS 300
QY 301 LELGWPSEVPSTLTVYSCHPSPRPAKRLQLTQELQEPALVESDGVKPSFWPTAQNCGG 360
DB 301 LELGWPSEVPSTLTVYSCHPSPRPAKRLQLTQELQEPALVESDGVKPSFWPTAQNCGG 360
QY 361 SAYSEERDRPYGLVSDITVTVLDAEGPCTWPCSCDDGYPALDLDAGLEPSPGLEDPDLD 420
DB 361 SAYSEERDRPYGLVSDITVTVLDAEGPCTWPCSCDDGYPALDLDAGLEPSPGLEDPDLD 420
QY 421 AGTTVLSGCVSAGSPGLGGPLGSLDLRLKPLADGEDWAGGLPWGGRSPGVSESEAGS 480
DB 421 AGTTVLSGCVSAGSPGLGGPLGSLDLRLKPLADGEDWAGGLPWGGRSPGVSESEAGS 480
QY 481 PLAGLDMDTFDSGFGVSDCSSPVECDFTSPGDEGPPRSYLQWVVIPIPLSSPGQAS 538

QY 121 APPENVTFSGQYNI SWRSYEDPAFYMLKGKLOLYQYRNRGDPWAVSPRRKLIISVDS 180
DB 121 APPENVTFSGQYNI SWRSYEDPAFYMLKGKLOLYQYRNRGDPWAVSPRRKLIISVDS 180
QY 181 RSVSLLPLEFRKDSSEYELQVRAGMPGSSYQGTWSEWSDPVI FQTQSEELKEGWNPHLLL 240
DB 181 RSVSLLPLEFRKDSSEYELQVRAGMPGSSYQGTWSEWSDPVI FQTQSEELKEGWNPHLLL 240
QY 241 LLLLVIVTIPAFWSIKTHPLWRLWKIWA VSPERFFMPLKYGCGSDPKKWWGAPFTGSS 300
DB 241 LLLLVIVTIPAFWSIKTHPLWRLWKIWA VSPERFFMPLKYGCGSDPKKWWGAPFTGSS 300
QY 301 LELGWSPEVPSTLEVYSCHPSPSAKRLQLTQELQEPALVESDCVPKPSFWPMTAQNSSG 360
DB 301 LELGWSPEVPSTLEVYSCHPSPSAKRLQLTQELQEPALVESDCVPKPSFWPMTAQNSSG 360
QY 361 SAYSEERDRPYGLVSDITVTVLDAEGPCTWPCSCDDGYPALDLDAGLEPSGLEDPILLD 420
DB 361 SAYSEERDRPYGLVSDITVTVLDAEGPCTWPCSCDDGYPALDLDAGLEPSGLEDPILLD 420
QY 421 ACTTVLSCGCVSAGSPGLGPGISLLDLKPLPLADGEDWAGLPGWGRSPGVSESEAGS 480
DB 421 ACTTVLSCGCVSAGSPGLGPGISLLDLKPLPLADGEDWAGLPGWGRSPGVSESEAGS 480
QY 481 PLAGLDMOTFDSGFVGCSSPVECDFTSPGDEGPPRSVLRQWVVI PPLSPGPGQAS 538
DB 481 PLAGLDMOTFDSGFVGCSSPVECDFTSPGDEGPPRSVLRQWVVI PPLSPGPGQAS 538
RESULT 5
AYY79312
ID AAY79312 standard; protein; 538 AA.
AC AAY79312;
DT 18-JUL-2000 (first entry)
XX Human cytokine receptor zalphall.
XX Cytokine receptor; zalphall; human; chromosome 16p11.1; apoptosis;
KW signal transduction; growth factor; cancer; tumour; infection;
KW immunosuppressive; immunostimulant; autoimmune disease; leukaemia;
KW lymphoma; transplant rejection; therapy; diagnosis.
XX Homo sapiens.
OS
FH Key
FT Peptide
FT Protein
FT Location/Qualifiers
1. .19
/note= "signal peptide"
20. .538
/note= "mature protein; a polypeptide comprising the
mature protein is specifically claimed in Claim 27(d)"
20. .237
/note= "cytokine-binding domain; a polypeptide comprising
this domain is specifically claimed in Claim 27(a)"
192. .202
/note= "penultimate strand region"
214. .218
/note= "WSXWS motif"
238. .255
/note= "transmembrane domain"
256. .538
/note= "intracellular signalling domain; a polypeptide
comprising this domain is specifically claimed in Claim
27(c)"
267. .273
/note= "Box I signalling site"
301. .304
/note= "Box II signalling site"
WO200017235-A2.
XX

PD 30-MAR-2000.
XX 23-SEP-1999; 99WO-US022149.
XX 23-SEP-1998; 98US-00159254.
PR 09-MAR-1999; 99US-00265117.
PR 06-JUL-1999; 99US-00347930.
XX (ZYMO) ZYMOGENETICS INC.
XX Presnell SR, Conklin DC, Novak JE, Hammond AK;
FI WPI; 2000-292825/25.
XX N-PSDB; AAZ94533, AAZ94534.
DR Novel nucleic acid encoding zalphall polypeptide, useful for treating
XX e.g. viral infection or tumors, and for identifying ligands that
XX stimulate cell proliferation.
PS Claim 27(e); Page 148-149; 190pp; English.
XX The present sequence is that of zalphall, a novel human class I cytokine
CC receptor that may be involved in an apoptotic cellular pathway, or is a
CC cell-cell signalling molecule, growth factor receptor, or extracellular
CC matrix associated protein with growth factor hormone activity. The
CC sequence was deduced from a cDNA clone (see AAZ94533) isolated from a
CC spinal cord library. Polypeptides comprising amino acids 20-237, 20-255,
CC 256-538, and 1-538 of the present sequence are claimed. Zalphall
CC is expressed in lymph node, peripheral blood leucocytes, spleen and
CC thymus. The mRNA is also abundant in the Raji cell line (ATCC CCL 86)
CC derived from Burkitt's lymphoma. Zalphall polypeptides, and fusion
CC proteins including them, can be obtained by expression in recombinant
CC host cells. They are used: to detect ligands (also ligand agonists and
CC antagonists) that stimulate proliferation and/or development of
CC haematopoietic, lymphoid and myeloid cells, in vitro or in vivo, e.g. as
CC a replacement for serum in culture media; to detect ligand-expressing cancers; to
CC activity (direct antagonists) and to detect ligand-expressing cancers; to
CC raise specific antibodies; and for purification of cognate ligands.
CC Agonistic ligands may stimulate cell-mediated immunity, e.g. for treating
CC (viral) infections associated with immunosuppression, improving the
CC activity of vaccines, suppressing tumours, treating leukaemia and
CC improving T-cell regeneration after bone marrow transplant. Antagonists
CC are useful as immunosuppressants, e.g. in the treatment of autoimmune
CC disease (e.g. rheumatoid arthritis, multiple sclerosis, diabetes), to
CC prevent transplant rejection and to treat T-cell leukemia or lymphoma
XX
SQ Sequence 538 AA;
Query Match 100.0%; Score 2958; DB 3; Length 538;
Best Local Similarity 100.0%; Pred. No. 6.2e-240;
Matches 538; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 MPRGWAAPLLLLLQGGWGPCDLVCYTDYLTQTVICILEMNLHPSTLTLTWQDQYEELKD 60
DB 1 MPRGWAAPLLLLLQGGWGPCDLVCYTDYLTQTVICILEMNLHPSTLTLTWQDQYEELKD 60
QY 61 EATCSLHRSAHNATHATYTCMDVHFHMADDIFSVNITDQSGNYSCGCSFLAESTKP 120
DB 61 EATCSLHRSAHNATHATYTCMDVHFHMADDIFSVNITDQSGNYSCGCSFLAESTKP 120
QY 121 APPENVTFSGQYNI SWRSYEDPAFYMLKGKLOLYQYRNRGDPWAVSPRRKLIISVDS 180
DB 121 APPENVTFSGQYNI SWRSYEDPAFYMLKGKLOLYQYRNRGDPWAVSPRRKLIISVDS 180
QY 181 RSVSLLPLEFRKDSSEYELQVRAGMPGSSYQGTWSEWSDPVI FQTQSEELKEGWNPHLLL 240
DB 181 RSVSLLPLEFRKDSSEYELQVRAGMPGSSYQGTWSEWSDPVI FQTQSEELKEGWNPHLLL 240
QY 241 LLLLVIVTIPAFWSIKTHPLWRLWKIWA VSPERFFMPLKYGCGSDPKKWWGAPFTGSS 300
DB 241 LLLLVIVTIPAFWSIKTHPLWRLWKIWA VSPERFFMPLKYGCGSDPKKWWGAPFTGSS 300
QY 301 LELGWSPEVPSTLEVYSCHPSPSAKRLQLTQELQEPALVESDCVPKPSFWPMTAQNSSG 360

Db 301 LELGWPSPVSTLEVSCHPRSPAKRLQLTELEPAELVESDGVPRSFPTQNSGG 360
Qy 361 SAYSEERDRPYGLVSDITVTLDAEGPCTWPCSCDDGYPALDLDALESPSPGLDPLLD 420
Db 361 SAYSEERDRPYGLVSDITVTLDAEGPCTWPCSCDDGYPALDLDALESPSPGLDPLLD 420
Qy 421 AGTTVLSCCVSAGSPGLGPGSLDLRLKPLADGEDWAGLPGWGRSPGVSESEAGS 480
Db 421 AGTTVLSCCVSAGSPGLGPGSLDLRLKPLADGEDWAGLPGWGRSPGVSESEAGS 480
Qy 481 PLAGLDMDTFDSGFVSGDCSSPVCECDFTSPGDEGPPRSYLRQWVIPPPLSSPGQAS 538
Db 481 PLAGLDMDTFDSGFVSGDCSSPVCECDFTSPGDEGPPRSYLRQWVIPPPLSSPGQAS 538

RESULT 6
ID AAB48001
XX AAB48001 standard; protein; 538 AA.
AC AAB48001;
XX
DT 19-MAR-2001 (first entry)
XX
DE Human IL-9/IL-2 receptor-like 16445 protein.
XX
KW Interleukin-9; IL-9; IL-2 receptor; 16445 protein; inflammatory;
KW T-lymphocyte-related disorder; antiarthritic; antipsoaritic; human;
KW immunoosuppressive; antiaesthetic; antiallergic; antithyroid; cytostatic;
KW antidiarrheic; nephrotropic; gene therapy.
XX
OS Homo sapiens.
XX
FH Key Location/Qualifiers
FT Peptide 1..19
FT Protein /note= "eignal peptide"
FT /note= "mature protein"
XX
WO200069880-A1.
XX
PD 23-NOV-2000.
XX
PF 18-MAY-2000; 2000WO-US013687.
XX
PR 18-MAY-1999; 99US-00313913.
XX
PA (MILL-) MILLENNIUM PHARM INC.
XX
PI Hodge MR;
XX
WPI; 2001-016209/02.
XX
DR N-PSDB; AAC84147.
XX
XX Novel interleukin-9/interleukin-2 receptor-like polypeptides useful for
PT diagnosis and treatment of immune, inflammatory and respiratory disorders
PT and in screening assays for identifying modulators.
XX
PS Claim 8; Page 104-106; 119pp; English.
XX

CC The invention relates to isolated human and murine interleukin-9 (IL-9)
CC /IL-2 receptor-like polypeptides. The plasmid containing the encoding
CC cDNA insert is deposited as ATCC PTA-350. The IL-9/IL-2 receptor-like
CC polypeptides (16445 proteins) can be recombinantly produced using
CC standard recombinant methodology. The 16445 proteins are used for
CC identifying their modulators and for diagnosis and treatment of immune,
CC inflammatory and respiratory disorders and disorders associated with
CC lungs, colon, kidney and lymphoid tissues including tonsil and thymus, in
CC particular T-lymphocyte-related disorders including atopic conditions
CC such as asthma, allergy, rheumatoid arthritis, psoriasis, chronic
CC inflammatory diseases and graft versus host disease, disorders involving
CC the colon such as diarrhoea, dysentery, infectious enterocolitis, kidney
CC disorders including polycystic kidney disease, cystic renal dysplasia,

CC disorders of the thymus including lymphomas, Hodgkin disease and
CC carcinoids. The 16445 polypeptides are also useful as modulating agents
CC in cellular processes including growth promoting activity, particularly
CC the antigen-independent proliferation of T-helper cell clones. The
CC encoding nucleic acid is useful as primers or hybridization probes for
CC the detection of IL-9/IL-2 receptor-like encoding nucleic acids and for
CC tissue typing and in forensic biology. The present sequence represents
CC the human IL-9/IL-2 receptor-like polypeptide (AAH16445)
XX
SQ Sequence 538 AA;
Query Match 100.0%; Score 2958; DB 4; Length 538;
Best Local Similarity 100.0%; Pred. No. 6.2e-240;
Matches 538; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 MPRGWAAPLLLLLQGGWGPCDLCVCTDYLTQVICILEMNNLHPSTLTLTWQDQYEELKD 60
Db 1 MPRGWAAPLLLLLQGGWGPCDLCVCTDYLTQVICILEMNNLHPSTLTLTWQDQYEELKD 60
Qy 61 EATCSLHRSAHNATHATYTCMDVHFHMADDIFSVNITDQSGNYSQCGSFLAESIKP 120
Db 61 EATCSLHRSAHNATHATYTCMDVHFHMADDIFSVNITDQSGNYSQCGSFLAESIKP 120
Qy 121 APPFNVTTFSGQYNISWRSYEDPAFYMLKGLQYELQYRNRGDPWAVSPRKLISVDS 180
Db 121 APPFNVTTFSGQYNISWRSYEDPAFYMLKGLQYELQYRNRGDPWAVSPRKLISVDS 180
Qy 181 RVSLLPLEFRKDSSEYELQVRAGMPGSSYQGTWSESDPVIQTQSEELKEGWNPHLL 240
Db 181 RVSLLPLEFRKDSSEYELQVRAGMPGSSYQGTWSESDPVIQTQSEELKEGWNPHLL 240
Qy 241 LLLLVIVIPAFWSLTKTHPLWRLWKIWAIVSPERFPMPLYKGCSDGFKKWWGAPFTGSS 300
Db 241 LLLLVIVIPAFWSLTKTHPLWRLWKIWAIVSPERFPMPLYKGCSDGFKKWWGAPFTGSS 300
Qy 301 LELGWPSPVSTLEVSCHPRSPAKRLQLTELEPAELVESDGVPRSFPTQNSGG 360
Db 301 LELGWPSPVSTLEVSCHPRSPAKRLQLTELEPAELVESDGVPRSFPTQNSGG 360
Qy 361 SAYSEERDRPYGLVSDITVTLDAEGPCTWPCSCDDGYPALDLDALESPSPGLDPLLD 420
Db 361 SAYSEERDRPYGLVSDITVTLDAEGPCTWPCSCDDGYPALDLDALESPSPGLDPLLD 420
Qy 421 AGTTVLSCCVSAGSPGLGPGSLDLRLKPLADGEDWAGLPGWGRSPGVSESEAGS 480
Db 421 AGTTVLSCCVSAGSPGLGPGSLDLRLKPLADGEDWAGLPGWGRSPGVSESEAGS 480
Qy 481 PLAGLDMDTFDSGFVSGDCSSPVCECDFTSPGDEGPPRSYLRQWVIPPPLSSPGQAS 538
Db 481 PLAGLDMDTFDSGFVSGDCSSPVCECDFTSPGDEGPPRSYLRQWVIPPPLSSPGQAS 538

RESULT 7
AAB81960
ID ABB81960 standard; protein; 538 AA.
XX
AC ABB81960;
XX
DT 25-NOV-2002 (first entry)
XX
DE Human 16445 protein.
XX
KW Interleukin; IL-9; IL-2; 16445; antiaesthetic; antiallergic; human;
KW antipsoaritic; antiinflammatory; immunoosuppressive; cytostatic; virucide;
KW antirheumatic; antiarthritic; antidiabetic; antithyroid; dermatological;
KW nephrotropic; antibacterial; tuberculoostatic; antileprotic; antipyrretic;
KW antiulcer; gene therapy; receptor.
XX
OS Homo sapiens.
XX
PN US2002090680-A1.
XX
PD 11-JUL-2002.

XX	26-SEP-2001; 2001US-00965313.	QY	421	AGTTVLSGCVSAGSPGLGGPLGSLDLRLKPLADGEDWAGGLPWGGRSPGVSESEAGS	480
PF		Db	421	AGTTVLSGCVSAGSPGLGGPLGSLDLRLKPLADGEDWAGGLPWGGRSPGVSESEAGS	480
XX					
PR	18-MAY-1999; 99US-00313913.				
PR	18-MAY-2000; 2000US-00574100.				
XX					
PA	(MILL-) MILLENNIUM PHARM INC.	QY	481	PLAGLDMDTDFSGFVGSDCSPVECDFTSPGDEGPPRSYLRQWVVIPLPSSPGPQAS	538
XX		Db	481	PLAGLDMDTDFSGFVGSDCSPVECDFTSPGDEGPPRSYLRQWVVIPLPSSPGPQAS	538
PI					
XX	Hodge MR;				
XX					
DR	WPI; 2002-655832/70.	RESULT 8			
DR	N-PSDB; ABQ79536.	AAU11912			
XX		ID	AAU11912	standard; protein; 538 AA.	
XX		XX	XX		
PT	New interleukin-9/interleukin-2 receptor-like polypeptides and	AC	AAU11912;		
PT	polynucleotides for diagnosing, treating respiratory, T-lymphocyte	XX			
PT	related disorders and disorders associated with lung, colon, kidney and	DT	09-APR-2002 (first entry)		
PT	lymphoid tissues.	XX			
XX		DE	Human MU-1 haematopoietin receptor superfamily chain protein sequence.		
PS	Claim 8; Page 31-33; 54pp; English.	XX			
XX		KW	Human; MU-1; haematopoietin receptor superfamily chain; thyroiditis;		
CC	The invention relates to isolated interleukin (IL)-9/IL-2 receptor-like	KW	immune deficiency; anaemia; autoimmune disorder; multiple sclerosis;		
CC	polypeptide, 16445. The 16445 polypeptides can be expressed by standard	KW	systemic lupus erythematosus; rheumatoid arthritis;		
CC	recombinant methodology. The 16445 polypeptide, polynucleotides and their	KW	pulmonary inflammation; insulin dependent diabetes mellitus;		
CC	modulators are useful for modulating the immune, inflammatory and	KW	nutritional supplement; cytokine receptor family.		
CC	respiratory responses, for the diagnosis and treatment of immune and	XX			
CC	respiratory disorders, particularly for the treatment and diagnosis of T-	OS	Homo sapiens.		
CC	lymphocyte-related disorders, including, atopic conditions, such as	XX			
CC	asthma and allergy, including allergic rhinitis, psoriasis, the effects	XX			
CC	of pathogen infection, chronic inflammatory diseases, organ-specific	FH	Key	Location/Qualifiers	
CC	autoimmunity, graft rejection, and graft versus host disease. The	FT	Domain	237. .254	
CC	molecules are also useful as modulating agents in a variety of cellular	FT	/note= "Transmembrane domain"		
CC	processes including growth promoting activity, particularly the antigen	XX			
CC	independent proliferation of T helper cell clones, and direct effects on	PN	WO200185792-A2.		
CC	normal haemopoietic progenitors, human T cells, B cells, thymocytes,	XX			
CC	thymic lymphomas and neuronal cell lines. They are useful for the	PD	15-NOV-2001.		
CC	modulation, diagnosis, and treatment of immune, inflammatory, and	PF	11-MAY-2001; 2001WO-US015395.		
CC	respiratory disorders and disorders associated with lungs, colon, kidney,	XX			
CC	and lymphoid tissues including tonsil and thymus. The present sequence	PR	05-NOV-1999; 99US-00569384.		
CC	represents a human 16445 polypeptide	XX	(GEMY) GENETICS INST INC.		
XX		XX			
SQ	Sequence 538 AA;	PI	Donaldson DD, Unger MJ, Young DA, Whitters MJ, Lowe L, Collins M;		
	Query Match 100.0%; Score 2958; DB 5; Length 538;	XX			
	Best Local Similarity 100.0%; Pred. No. 6.2e-240;	XX			
	Matches 538; Conservative 0; Mismatches 0; Indels 0; Gaps 0;	DR	WPI; 2002-062239/08.		
		DR	N-PSDB; AAS17248.		
QY	1 MPRGWAAPLLLLLGGGCGPDLVCYDYLQTVICILEMNLHPSTLTLTWQDQYEELKD 60	XX			
Db	1 MPRGWAAPLLLLLGGGCGPDLVCYDYLQTVICILEMNLHPSTLTLTWQDQYEELKD 60	PT	New polypeptide, useful for identifying compounds binding to MU-1, and		
		PT	for treating multiple sclerosis, rheumatoid arthritis, diabetes and		
QY	61 EATSCSLHRSANAHATYTCMDYVHFHMADDFSVNITDQSGNYSQCGSFLLAESIKP 120	PT	asthma, comprises the isolated murine MU-1 protein, and a hematopoietin		
Db	61 EATSCSLHRSANAHATYTCMDYVHFHMADDFSVNITDQSGNYSQCGSFLLAESIKP 120	XX	receptor superfamily chain.		
		XX			
QY	121 APPFNVTTFSGQYNISRWSDYEDAFYMLKGKQLQYELQYRNRGDPWAPSPRKLISVDS 180	PS	Disclosure; Fig 4; 59pp; English.		
Db	121 APPFNVTTFSGQYNISRWSDYEDAFYMLKGKQLQYELQYRNRGDPWAPSPRKLISVDS 180	CC	The present invention relates to a new murine MU-1 protein, a		
		CC	haematopoietin receptor superfamily chain, comprising a fully defined		
QY	181 RVSLLPLEFRKDSYELQVRAGMPGSSYQGTWSESDPVIQTQSEELKEGWNPHLLL 240	CC	sequence of 529 amino acids (AAU1915) as given in the specifications or		
Db	181 RVSLLPLEFRKDSYELQVRAGMPGSSYQGTWSESDPVIQTQSEELKEGWNPHLLL 240	CC	fragment of protein having MU-1 biological activity. The molecules of the		
		CC	invention may exhibit cytokine, cell proliferation or cell		
QY	241 LLLLIVIFTPAFWSLKTHPLWRLWKKIWAVSPERFFMPLKGCSDGDKWVGAPFTGSS 300	CC	differentiation activity and may also exhibit immune stimulating or		
Db	241 LLLLIVIFTPAFWSLKTHPLWRLWKKIWAVSPERFFMPLKGCSDGDKWVGAPFTGSS 300	CC	immune suppressing activity and can be useful in the treatment of various		
		CC	immune deficiencies and disorders including severe combined		
QY	301 LELGWPSPVPSTLEVYSCHPSPRSPAKRLQLTELQEPALVESDGVPPKSPFWPTAQNCGG 360	CC	immunodeficiency (SCID). Another use of the invention is treating		
Db	301 LELGWPSPVPSTLEVYSCHPSPRSPAKRLQLTELQEPALVESDGVPPKSPFWPTAQNCGG 360	CC	autoimmune disorders such as connective tissue disease, multiple		
		CC	sclerosis, systemic lupus erythematosus, rheumatoid arthritis, autoimmune		
QY	361 SAYSEERDRPYGLVSDITVTVLDAEGPCTWPCSCDDGYPALDLDAGLEPSPGLBPLLD 420	CC	pulmonary inflammation, autoimmune thyroiditis, insulin dependent		
Db	361 SAYSEERDRPYGLVSDITVTVLDAEGPCTWPCSCDDGYPALDLDAGLEPSPGLBPLLD 420	CC	diabetes mellitus, and autoimmune inflammatory eye disease. The invention		
		CC	is useful for the treatment of myeloid or lymphoid cell deficiencies and		
		CC	in treating various anemias or for use in conjunction with		
		CC	irradiation/chemotherapy to stimulate the production of erythroid		
		CC	precursors and/or erythroid cells. the polynucleotides and proteins can		
		CC	also be used as nutritional sources or supplements. The present protein		
		CC	sequence represents the human MU-1 haematopoietin receptor superfamily		

CC chain. MU-1 is also a member of the cytokine receptor family. This
CC sequence was used in the invention for the characterisation of previously
CC unknown members of the haematopoietin receptor superfamily
XX
SQ Sequence 538 AA;

Query Match 100.0%; Score 2958; DB 5; Length 538;
Best Local Similarity 100.0%; Pred. No. 6.2e-240; Indels 0; Gaps 0;
Matches 538; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 MPRGWAAPLLLLLLQGGWCPDLVCYTDYLTQVICILEMNLHPSTLTLTWQDQYEELKD 60
Db 1 MPRGWAAPLLLLLLQGGWCPDLVCYTDYLTQVICILEMNLHPSTLTLTWQDQYEELKD 60
QY 61 EATSCSLHSAHNATHATYTCMDVHFHMADDFSVNITDQSGNYSCQSGSFLAESIKP 120
Db 61 EATSCSLHSAHNATHATYTCMDVHFHMADDFSVNITDQSGNYSCQSGSFLAESIKP 120
QY 121 APPFNVTTFSGQYNISWRSDYEDPAFYMLKGKIQYELQYRNRGDPWAVSPRKLISVDS 180
Db 121 APPFNVTTFSGQYNISWRSDYEDPAFYMLKGKIQYELQYRNRGDPWAVSPRKLISVDS 180
QY 181 RSVSLLPLEFRKDSYVELQVRAGMPGSSYQGTWSEWSDPVIFQTSBELKEGWNPHLLL 240
Db 181 RSVSLLPLEFRKDSYVELQVRAGMPGSSYQGTWSEWSDPVIFQTSBELKEGWNPHLLL 240
QY 241 LLLLIVVTFAPFWSLKTPLMLWKKIWAVSPERFFMPLYKGCSDGPKKWVGAPFTGSS 300
Db 241 LLLLIVVTFAPFWSLKTPLMLWKKIWAVSPERFFMPLYKGCSDGPKKWVGAPFTGSS 300
QY 301 LELGWSPEVPSTLEYSCHPRSPAKRLQLTELQEPALVESDGVKPSFWPTAQNSGG 360
Db 301 LELGWSPEVPSTLEYSCHPRSPAKRLQLTELQEPALVESDGVKPSFWPTAQNSGG 360
QY 361 SAYSERDRPYGLVSTDTVTVDAGPCTWPCSDGDPALDLAGLEPSGLDPLLD 420
Db 361 SAYSERDRPYGLVSTDTVTVDAGPCTWPCSDGDPALDLAGLEPSGLDPLLD 420
QY 421 ACTTVLSCGCVSAGSPLGGLSLDLRLKPLADGEDWAGGLPWGGRSPGVSEAGS 480
Db 421 ACTTVLSCGCVSAGSPLGGLSLDLRLKPLADGEDWAGGLPWGGRSPGVSEAGS 480
QY 481 PLAGLDMTDFDSGFGVSDCSSPVECDFTSPGDEGPPRSYLRQWVIPPPLSPGQAS 538
Db 481 PLAGLDMTDFDSGFGVSDCSSPVECDFTSPGDEGPPRSYLRQWVIPPPLSPGQAS 538

RESULT 9

AAE13726
ID AAE13726 standard; protein; 538 AA.

AAE13726;

26-FEB-2002 (first entry)

Human soluble Zalphall cytokine receptor protein.

Human; Zalphall; cytokine receptor; immunosuppressive; cytostatic;
inflammatory disorder; haemostatic; cell proliferation; immune disorder;
autoimmune disease; rheumatoid arthritis; multiple sclerosis; cancer;
myaethenia gravis; systemic lupus erythematosus; SLE; diabetes; asthma;
ulcerative colitis; inflammatory bowel disease; Crohn's disease; sepsis;
viral infection.

Homo sapiens.

Key Location/Qualifiers

FT Peptide 1..19

FT Protein 20..538 /label= Signal_peptide

FT Protein /label= Mature_Zalphall_protein

FT Domain 20..237

FT /label= Cytokine_binding_domain

FT Domain 120..123
FT /label= Domain_linker
FT Region 192..202
FT /note= "penultimate strand region"
FT Domain 214..218
FT /note= "WSXWS motif"
FT Domain 238..255
FT /label= Transmembrane_domain
FT Domain 256..538
FT /label= Intracellular_signalling_domain
FT Region 267..273
FT /note= "Box I signalling site"
FT Region 301..304
FT /note= "Box II signalling site"
FT Binding-site 519..522
FT /label= STAT3_binding_site
PN WO200177171-A2.
XX
XX 18-OCT-2001.
XX 03-APR-2001; 2001WO-US010872.
XX 05-APR-2000; 2000US-0194731P.
XX 28-JUL-2000; 2000US-0222121P.
XX (ZYMO) ZYMOGENETICS INC.
XX
XX Sprecher CA, Novak JE, West JW, Presnell SR, Holly RD, Nelson AJ;
WPI; 2002-025898/03.
DR N-PSDB; AAD22918.
XX
XX Novel soluble receptor polypeptides and polynucleotides used as cytokine
XX antagonist for stimulating ligand activity-induced proliferation of
XX hematopoietic cells and for suppressing immune response in a mammal.
PS Example 1; Page 172-173; 243pp; English.
XX
XX The invention relates to an isolated soluble zalphall cytokine receptor
XX polypeptide and their cDNA molecules. Zalphall proteins are useful for
XX inhibiting or antagonising the ligand activity-induced proliferation of
XX haematopoietic cells and haematopoietic cell progenitors preferably
XX lymphoid cells which are natural killer cells or cytotoxic T cells.
XX Zalphall is useful for treating immune and inflammatory disorders, for
XX reducing proliferation of neoplastic B or T cells, for suppressing an
XX immune response in a mammal exposed to an antigen or pathogen. Zalphall is
XX useful for treating diseases that require immune regulation including
XX autoimmune diseases such as rheumatoid arthritis, multiple sclerosis,
XX myaethenia gravis, systemic lupus erythematosus (SLE) and diabetes;
XX asthma, ulcerative colitis, inflammatory bowel disease, Crohn's disease,
XX sepsis, viral infection (dengue virus infection) and cancer. The present
XX sequence is human soluble Zalphall cytokine receptor protein
SQ Sequence 538 AA;
Query Match 100.0%; Score 2958; DB 5; Length 538;
Best Local Similarity 100.0%; Pred. No. 6.2e-240;
Matches 538; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 MPRGWAAPLLLLLLQGGWCPDLVCYTDYLTQVICILEMNLHPSTLTLTWQDQYEELKD 60
Db 1 MPRGWAAPLLLLLLQGGWCPDLVCYTDYLTQVICILEMNLHPSTLTLTWQDQYEELKD 60
QY 61 EATSCSLHSAHNATHATYTCMDVHFHMADDFSVNITDQSGNYSCQSGSFLAESIKP 120
Db 61 EATSCSLHSAHNATHATYTCMDVHFHMADDFSVNITDQSGNYSCQSGSFLAESIKP 120
QY 121 APPFNVTTFSGQYNISWRSDYEDPAFYMLKGKIQYELQYRNRGDPWAVSPRKLISVDS 180
Db 121 APPFNVTTFSGQYNISWRSDYEDPAFYMLKGKIQYELQYRNRGDPWAVSPRKLISVDS 180
QY 181 RSVSLLPLEFRKDSYVELQVRAGMPGSSYQGTWSEWSDPVIFQTSBELKEGWNPHLLL 240

Db 181 RSVLLPLEFRKDSYELQVRAGPFGSSYQGTWSESDPVIQTQSEELKEGWNPHLL 240
Qy 241 LLLLVIVIFAPWSLKTPLRLWKIWA VSPERFPMPLVKGSGDFKWKVGAPFTGSS 300
Db 241 LLLLVIVIFAPWSLKTPLRLWKIWA VSPERFPMPLVKGSGDFKWKVGAPFTGSS 300
Qy 301 LELGWSPEVPSTLEVYCHPPSPAKRLQLTQELQEPALVESDGVKPKSPFWPTAQNSSG 360
Db 301 LELGWSPEVPSTLEVYCHPPSPAKRLQLTQELQEPALVESDGVKPKSPFWPTAQNSSG 360
Qy 361 SAYSEERDRPYGLVSDITVTVLDAEGPCTWPCSCDDGYPALDLADAGLEPSGLEDPLLD 420
Db 361 SAYSEERDRPYGLVSDITVTVLDAEGPCTWPCSCDDGYPALDLADAGLEPSGLEDPLLD 420
Qy 421 AGTTVLSCGCVSAGSPGLGGPLGSLDLRLKPLADGEDWAGGLPWGGRSPGVSESEAGS 480
Db 421 AGTTVLSCGCVSAGSPGLGGPLGSLDLRLKPLADGEDWAGGLPWGGRSPGVSESEAGS 480
Qy 481 PLAGLDMDTFDSGFVSGDCSSPVECDFTSPGDEGPPRSYLRQWVIPPPLSSPGPQAS 538
Db 481 PLAGLDMDTFDSGFVSGDCSSPVECDFTSPGDEGPPRSYLRQWVIPPPLSSPGPQAS 538

RESULT 10
AAU11978
XX AAU11978 standard; protein; 538 AA.
AC AAU11978;
XX
DT 09-APR-2002 (first entry)
XX Human zalphall receptor polypeptide.
XX Cytokine; zalphall ligand; zalphall receptor; NK cell progenitor;
XX natural killer cell proliferation; T-cell proliferation;
KW B-cell proliferation; anti-tumour response; immune system;
XX immunostimulant; cytostatic; human.
XX Homo sapiens.
XX
PN US6307024-B1.
XX
PD 23-OCT-2001.
XX
PF 09-MAR-2000; 2000US-00522217.
XX
PR 09-MAR-1999; 99US-0123547P.
PR 11-MAR-1999; 99US-0123904P.
PR 01-JUL-1999; 99US-0142013P.
XX
PA (ZYMO) ZYMOGENETICS INC.
XX
XX Novak JE, Presnell SR, Sprecher CA, Foster DC, Holly RD;
PI Gross JA, Johnston JV, Nelson AJ, Dillon SR, Hammond AK;
XX
DR WPI: 2002-040208/05.
DR N-PSDB; AAS20642.
XX
XX New zalphall ligand polypeptides and polynucleotides, useful for
PT stimulating proliferation, activation, differentiation and/or induction
PT of inhibition of specialized cell function, or for stimulating an
PT antigenic response.
XX
XX Claim 1; Col 191-194; 105pp; English.
XX
XX The present invention relates to the isolation of a novel cytokine,
CC zalphall ligand and the polynucleotide encoding it. The invention also
CC gives the sequence for the zalphall receptor and the polynucleotide
CC encoding it. The zalphall ligand polypeptide stimulates proliferation of
CC natural killer (NK) cells or NK cell progenitors, the activation of NK
CC cells, proliferation of T-cells, proliferation of B-cells stimulated with
CC anti-CD40 antibodies, stimulates an antigenic response in a mammal, and

CC reduces proliferation of B-cells stimulated with anti-igm antibodies. The
CC zalphall ligand polypeptide is also useful in preparing antibodies that
CC bind to zalphall Ligand epitopes. The zalphall Ligand polynucleotides can
CC be used as probes or primers to clone regions of a zalphall Ligand gene,
CC and in gene therapy. Zalphall Ligand may also be used to identify
CC inhibitors of its activity, to enhance the generation of anti-tumour
CC responses with or without the infusion of donor lymphocytes, and to
CC activate or stimulate the immune system. The present sequence represents
CC human zalphall receptor polypeptide
XX
SQ Sequence 538 AA;
Query Match 100.0%; Score 2958; DB 5; Length 538;
Best Local Similarity 100.0%; Pred. No. 6.2e-240;
Matches 538; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 MPRGWAAPLLLLLQGGWGPCDLYCYDYLTQVTCILEMNLHPSTLTLTWQDQYBELKD 60
Db 1 MPRGWAAPLLLLLQGGWGPCDLYCYDYLTQVTCILEMNLHPSTLTLTWQDQYBELKD 60
Qy 61 EATSCSLHRSAHNATHATYTCMDVHFHMADDIPFVNITDQSGNYSOCGSFLLAESIKP 120
Db 61 EATSCSLHRSAHNATHATYTCMDVHFHMADDIPFVNITDQSGNYSOCGSFLLAESIKP 120
Qy 121 APPENVTVTFSGQYNIISWRSDYEDPAFYMLKGKLQYELQYRNRGDPWAVSPRKLISVDS 180
Db 121 APPENVTVTFSGQYNIISWRSDYEDPAFYMLKGKLQYELQYRNRGDPWAVSPRKLISVDS 180
Qy 181 RVSLLPLEFRKDSYELQVRAGPFGSSYQGTWSESDPVIQTQSEELKEGWNPHLL 240
Db 181 RVSLLPLEFRKDSYELQVRAGPFGSSYQGTWSESDPVIQTQSEELKEGWNPHLL 240
Qy 241 LLLLVIVIFAPWSLKTPLRLWKIWA VSPERFPMPLVKGSGDFKWKVGAPFTGSS 300
Db 241 LLLLVIVIFAPWSLKTPLRLWKIWA VSPERFPMPLVKGSGDFKWKVGAPFTGSS 300
Qy 301 LELGWSPEVPSTLEVYCHPPSPAKRLQLTQELQEPALVESDGVKPKSPFWPTAQNSSG 360
Db 301 LELGWSPEVPSTLEVYCHPPSPAKRLQLTQELQEPALVESDGVKPKSPFWPTAQNSSG 360
Qy 361 SAYSEERDRPYGLVSDITVTVLDAEGPCTWPCSCDDGYPALDLADAGLEPSGLEDPLLD 420
Db 361 SAYSEERDRPYGLVSDITVTVLDAEGPCTWPCSCDDGYPALDLADAGLEPSGLEDPLLD 420
Qy 421 AGTTVLSCGCVSAGSPGLGGPLGSLDLRLKPLADGEDWAGGLPWGGRSPGVSESEAGS 480
Db 421 AGTTVLSCGCVSAGSPGLGGPLGSLDLRLKPLADGEDWAGGLPWGGRSPGVSESEAGS 480
Qy 481 PLAGLDMDTFDSGFVSGDCSSPVECDFTSPGDEGPPRSYLRQWVIPPPLSSPGPQAS 538
Db 481 PLAGLDMDTFDSGFVSGDCSSPVECDFTSPGDEGPPRSYLRQWVIPPPLSSPGPQAS 538

RESULT 11
ABR61402
ID ABR61402 standard; protein; 538 AA.
XX
AC ABR61402;
XX
DT 12-AUG-2003 (first entry)
XX
DE Human IL-21R SEQ ID NO:2.
XX
KW arthritic disorder; interleukin-21; IL-21; IL-21 receptor; IL-21R;
KW immune cell activity; cancer; infectious disorder; antirheumatic;
KW antiarthritic; osteopathic; antipsoriatic; cytostatic; antibacterial;
KW virucide; antiparasitic; immunosuppressive; antidiabetic; dermatological;
KW neuroprotective; antiulcer; antiallergic; antianaemic; hepatotropic;
KW antithyroid; antiinflammatory; immune response; immune disorder;
XX autoimmune disease; human.
XX Homo sapiens.
OS

PN WO2003028630-A2.
 XX 10-APR-2003.
 PD
 PF 04-OCT-2002; 2002WO-US029839.
 PP 04-OCT-2001; 2001US-00972218.
 PR 17-APR-2002; 2002US-0373746P.
 PX
 XX (AMHP) WYETH.
 PA
 XX Carter L, Whitters MJ, Collins M, Young DA, Larsen G;
 PI Donaldson DD, Lowe LD, Dunussi K, Ma M, Witek JS, Kasaian MT;
 PI Ungar M;
 XX
 DR WPI; 2003-430146/40.
 DR N-PSDB; ACC80861.
 XX
 XX Treating or preventing arthritic disorder, cancer or infectious disorders
 PT in a subject, involves administering a modulator of interleukin-21 or its
 PT receptor which modulate immune cell activity.
 XX
 PS Claim 40; Fig 2B; 176pp; English.
 XX
 CC The invention relates to a novel method for treating or preventing an
 CC arthritic disorder in a subject. The method involves administering to the
 CC subject an interleukin-21 (IL-21)/IL-21 receptor (IL-21R) antagonist
 CC optionally in combination with another therapeutic agent, to inhibit or
 CC reduce immune cell activity in the subject. The method is also useful for
 CC treating or preventing cancer or an infectious disorder, in a subject, by
 CC administering IL-21/IL-21R agonist, to increase immune cell activity. The
 CC method of the invention has antirheumatic, antiarthritic, osteopathic,
 CC antipsoriatic, cycostatic, antibacterial, virucide, antiparasitic,
 CC immunosuppressive, antidiabetic, neuroprotective, dermatological,
 CC antitumor, antiallergic, antianemic, hepatotropic,
 CC antithyroid, and antiinflammatory activity. The method is useful for
 CC treating or preventing an arthritic disorder such as rheumatoid
 CC arthritis, juvenile rheumatoid arthritis, osteoarthritis, psoriatic
 CC arthritis or ankylosing spondylitis, and also cancer such as solid
 CC tumour, soft tissue tumour or metastatic lesion, or an infectious
 CC disorder such as bacterial, viral or parasitic infection in a mammal,
 CC preferably human. A method of the invention is also useful for
 CC increasing the ability of a vaccine composition containing an antigen to
 CC elicit a protective immune response in a subject against the antigen.
 CC The antigen is from a pathogen such as virus, bacterium or protozoan, or
 CC from cancer or tumour cell antigen, or expressed on the surface of cancer
 CC cell. An alternative method of the invention is useful for modulating the
 CC activity of immune or haematopoietic cells and thus to treat or prevent a
 CC variety of immune disorders, such as autoimmune diseases, for example
 CC diabetes mellitus, multiple sclerosis, myasthenia gravis, systemic lupus
 CC erythematosus, dermatitis, ulcer, asthma, allergic asthma, anaemia,
 CC hepatitis, Graves's disease, graft versus host disease, and scleroderma.
 CC The present sequence is used in an exemplification of the invention
 XX
 SQ Sequence 538 AA;
 Query Match 100.0%; Score 2958; DB 6; Length 538;
 Best Local Similarity 100.0%; Pred. NO. 6.2e-240;
 Matches 538; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 MPRGWAAPLLLLLGGGCGCPDLVCYTDYLTQTVICILEMWNLPSTLTITWQDYELKD 60
 DB 1 MPRGWAAPLLLLLGGGCGCPDLVCYTDYLTQTVICILEMWNLPSTLTITWQDYELKD 60
 QY 61 EATSCSLHRSANATHATYTCMDVPHFWADDIFSVNITDQSGNTSQEGSFLLAESIKP 120
 DB 61 EATSCSLHRSANATHATYTCMDVPHFWADDIFSVNITDQSGNTSQEGSFLLAESIKP 120
 QY 121 APPFNVTTFSGQYNISMRSDYEDPAFYMLKGLQYELQYRNRPWAVSPRKLISVDS 180
 DB 121 APPFNVTTFSGQYNISMRSDYEDPAFYMLKGLQYELQYRNRPWAVSPRKLISVDS 180
 QY 181 RSVSLLPLEFRKDDSSYELQVRAGMPGSSYQGTWSENSDPVITFQTSSELKEGWNPHULL 240

DB 181 RSVSLLPLEFRKDDSSYELQVRAGMPGSSYQGTWSENSDPVITFQTSSELKEGWNPHULL 240
 QY 241 LLLLVIVFIPAFWSLTKTHPLMRLWKIWAIVSPERFFMPLYKGCSDGDFKKWVGAPFTGSS 300
 DB 241 LLLLVIVFIPAFWSLTKTHPLMRLWKIWAIVSPERFFMPLYKGCSDGDFKKWVGAPFTGSS 300
 QY 301 LELGWSPEVSTLEVYSCHPPRSPAKRLQLTELQEPALVELSDGVKPSFWPTQNSGG 360
 DB 301 LELGWSPEVSTLEVYSCHPPRSPAKRLQLTELQEPALVELSDGVKPSFWPTQNSGG 360
 QY 361 SAYSERDRPYGLVSDITVTVLDAEGPCTWPCSCDDGYPALDLDAGLEPSPGLGEDPLLD 420
 DB 361 SAYSERDRPYGLVSDITVTVLDAEGPCTWPCSCDDGYPALDLDAGLEPSPGLGEDPLLD 420
 QY 421 AGTTVLSGCVSAGSPGLGGLSLLDRLKPLADGEDWAGGLPWGGRSPGVSSEAGS 480
 DB 421 AGTTVLSGCVSAGSPGLGGLSLLDRLKPLADGEDWAGGLPWGGRSPGVSSEAGS 480
 QY 481 PLAGLDMDTFDSGFGVSDCSSPVECDFTSPGDEGPPRSYLRQWVITPPPLSSPGPQAS 538
 DB 481 PLAGLDMDTFDSGFGVSDCSSPVECDFTSPGDEGPPRSYLRQWVITPPPLSSPGPQAS 538
 RESULT 12
 AAEI4939
 ID AAEI4939 standard; protein; 538 AA.
 XX AAEI4939;
 DT 27-AUG-2003 (first entry)
 XX Human interleukin-21 (IL-21) receptor.
 DE Interleukin-21; antagonist; cancer; inflammatory; autoimmune disorder;
 KW rheumatoid arthritis; multiple sclerosis; systemic lupus erythematosus;
 KW myasthenia gravis; diabetes; human; zalphall receptor; IL-21 receptor.
 XX Homo sapiens.
 OS
 PN WO2003040313-A2.
 PD 15-MAY-2003.
 XX 28-OCT-2002; 2002WO-US034502.
 XX 05-NOV-2001; 2001US-0337586P.
 XX (ZYMO) ZYMOGENETICS INC.
 XX Presnell SR, West JW, Novak JE;
 XX WPI; 2003-441547/41.
 XX N-PSDB; AAD47859.
 XX
 PT New IL-21 polypeptide and encoding polynucleotide, useful for diagnosing
 PT and treating disorders with aberrant expression or activity of the IL-21
 PT polypeptide, such as cancer, rheumatoid arthritis, multiple sclerosis and
 PT diabetes.
 XX
 PS Example 1; Page 65-67; 71pp; English.
 XX
 CC The invention relates to polynucleotides and polypeptides of interleukin-
 CC 21 (IL-21) antagonists, that bind with specificity and exhibit an EC50
 CC that is not detectable in receptor binding studies. The antagonists of
 CC the invention have mutations in the D helix of the IL-21 molecule, and
 CC can be used to inhibit the activity of IL-21 with its cognate receptor.
 CC The IL-21 antagonists are useful for diagnosing and treating disorders
 CC involving the aberrant expression or activity of the IL-21 polypeptide,
 CC such as cancer, inflammatory and autoimmune disorders, including
 CC rheumatoid arthritis, multiple sclerosis, systemic lupus erythematosus,
 CC myasthenia gravis and diabetes. The polypeptides can also be used to
 CC prepare antibodies that bind IL-21 epitopes, peptides or polypeptides,

CC and for enhancing in vivo killing of target tissues. The present sequence
CC is human IL-21 receptor (originally designated zalphall1 receptor)
XX
SQ Sequence 538 AA;

Query Match 100.0%; Score 2958; DB 7; Length 538;
Best Local Similarity 100.0%; Pred. No. 6.2e-240;
Matches 538; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MPRGWAAPLLLLLQGGGCPDLVCYTDYLTQVICILEMNLHPSTLTLTWQDQVEELKD 60
DB 1 MPRGWAAPLLLLLQGGGCPDLVCYTDYLTQVICILEMNLHPSTLTLTWQDQVEELKD 60

QY 61 EATCSLHRSAHNATHATYTCMDVHFHMADDFSVNITDQSGNYSCGCSFLLAESIKP 120
DB 61 EATCSLHRSAHNATHATYTCMDVHFHMADDFSVNITDQSGNYSCGCSFLLAESIKP 120

QY 121 APPFNVTTFSGQYINISWRSDYEDPAFYMLKGKQLQYELQYRNRPDPAVSPRRKLISVDS 180
DB 121 APPFNVTTFSGQYINISWRSDYEDPAFYMLKGKQLQYELQYRNRPDPAVSPRRKLISVDS 180

QY 181 RVSLLPLEFRKDSYELQVRAGMPGSSYQGTWSEWSDPVIQTQSEELKEGWNPHLL 240
DB 181 RVSLLPLEFRKDSYELQVRAGMPGSSYQGTWSEWSDPVIQTQSEELKEGWNPHLL 240

QY 241 LLLLVIPTAFWSLTKTHPLWRLWKIWA VSPERFFMPLYKGCSDGFKKWWGAPFTGSS 300
DB 241 LLLLVIPTAFWSLTKTHPLWRLWKIWA VSPERFFMPLYKGCSDGFKKWWGAPFTGSS 300

QY 301 LELGWSPEVPSTLEVYSCHPPRSPAKRLQLTELQEPALVESDGVKPSFWPTAQN SGG 360
DB 301 LELGWSPEVPSTLEVYSCHPPRSPAKRLQLTELQEPALVESDGVKPSFWPTAQN SGG 360

QY 361 SAYSEERDRPYGLVSDITVTVDAGGCTWPCSCDDGYPALDLDAGLEPSGLDPLLD 420
DB 361 SAYSEERDRPYGLVSDITVTVDAGGCTWPCSCDDGYPALDLDAGLEPSGLDPLLD 420

QY 421 AGTTVLSCGVSAGSPGLGGLSLLDRKPLADGEDWAGGLPWGGRSPGVSESEAGS 480
DB 421 AGTTVLSCGVSAGSPGLGGLSLLDRKPLADGEDWAGGLPWGGRSPGVSESEAGS 480

QY 481 PLAGLDMDTFDSGFGSDCSSPVECDFTSPGDEGPPRSYLRQWVVI PPLSSPGQAS 538
DB 481 PLAGLDMDTFDSGFGSDCSSPVECDFTSPGDEGPPRSYLRQWVVI PPLSSPGQAS 538

RESULT 13

ABU62888

ID ABU62888 standard; protein; 538 AA.

XX AC ABU62888;

XX DT 15-SEP-2003 (first entry)

XX DE Human MU-1 haematopoietin receptor superfamily chain.

XX KW Human; MU-1; haematopoietin receptor superfamily chain; immunomodulator;

XX KW cytostatic; antibacterial; virucide; antianaemic; gene therapy;

XX KW haematopoiesis; anaemias; immune response; cancer; infection;

XX KW transplanted organ; cytokine; receptor.

XX OS Homo sapiens.

XX PN US2003049798-A1.

XX PD 13-MAR-2003.

XX PF 04-OCT-2001; 2001US-00972218.

XX PR 17-MAR-1998; 98US-00040005.

XX PR 28-APR-2000; 2000US-00560766.

XX PR 11-MAY-2000; 2000US-00569384.

XX XX

PA (CART/) CARTER L.
PA (WHIT/) WHITERS M J.
PA (COLL/) COLLINS M.
PA (YOUN/) YOUNG D A.
PA (DONA/) DONALDSON D D.
PA (LOWE/) LOWE L D.
PA (UNGE/) UNGER M.
XX
PI Carter L, Whitters MJ, Collins M, Young DA, Donaldson DD;
PI Lowe LD, Unger M;
XX
DR WPI; 2003-512354/48.
DR N-PSDB; ACD26717.
XX
PT New fusion polypeptide for regulating hematopoiesis and immune responses,
PT comprises a fragment of a MU-1 polypeptide and a non-MU-1 fusion
PT polypeptide.
XX
PS Claim 13; Fig 4; 26pp; English.

CC The invention describes a fusion polypeptide comprising at least a
CC fragment of a MU-1 polypeptide and a non-MU-1 fusion polypeptide. The
CC polypeptide is useful in regulating haematopoiesis (e.g. in cases of
CC anaemias) and/or immune responses (e.g. immune response to cancer,
CC infections or to a transplanted organ) and in identifying other members
CC of the haematopoietin superfamily, including cytokines and receptors. The
CC polynucleotide may be used to express recombinant protein for analysis,
CC characterisation or therapeutic use; and as markers for tissues or
CC chromosomes. The polypeptide and polynucleotide may also be used as
CC nutritional sources or supplements. This is the amino acid sequence of
CC human MU-1 haematopoietin receptor superfamily chain
XX
SQ Sequence 538 AA;

Query Match 100.0%; Score 2958; DB 7; Length 538;

Best Local Similarity 100.0%; Pred. No. 6.2e-240;

Matches 538; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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DB 61 EATCSLHRSAHNATHATYTCMDVHFHMADDFSVNITDQSGNYSCGCSFLLAESIKP 120

QY 121 APPFNVTTFSGQYINISWRSDYEDPAFYMLKGKQLQYELQYRNRPDPAVSPRRKLISVDS 180
DB 121 APPFNVTTFSGQYINISWRSDYEDPAFYMLKGKQLQYELQYRNRPDPAVSPRRKLISVDS 180

QY 181 RVSLLPLEFRKDSYELQVRAGMPGSSYQGTWSEWSDPVIQTQSEELKEGWNPHLL 240
DB 181 RVSLLPLEFRKDSYELQVRAGMPGSSYQGTWSEWSDPVIQTQSEELKEGWNPHLL 240

QY 241 LLLLVIPTAFWSLTKTHPLWRLWKIWA VSPERFFMPLYKGCSDGFKKWWGAPFTGSS 300
DB 241 LLLLVIPTAFWSLTKTHPLWRLWKIWA VSPERFFMPLYKGCSDGFKKWWGAPFTGSS 300

QY 301 LELGWSPEVPSTLEVYSCHPPRSPAKRLQLTELQEPALVESDGVKPSFWPTAQN SGG 360
DB 301 LELGWSPEVPSTLEVYSCHPPRSPAKRLQLTELQEPALVESDGVKPSFWPTAQN SGG 360

QY 361 SAYSEERDRPYGLVSDITVTVDAGGCTWPCSCDDGYPALDLDAGLEPSGLDPLLD 420
DB 361 SAYSEERDRPYGLVSDITVTVDAGGCTWPCSCDDGYPALDLDAGLEPSGLDPLLD 420

QY 421 AGTTVLSCGVSAGSPGLGGLSLLDRKPLADGEDWAGGLPWGGRSPGVSESEAGS 480
DB 421 AGTTVLSCGVSAGSPGLGGLSLLDRKPLADGEDWAGGLPWGGRSPGVSESEAGS 480

QY 481 PLAGLDMDTFDSGFGSDCSSPVECDFTSPGDEGPPRSYLRQWVVI PPLSSPGQAS 538
DB 481 PLAGLDMDTFDSGFGSDCSSPVECDFTSPGDEGPPRSYLRQWVVI PPLSSPGQAS 538

RESULT 14

ABW00881

ID ABW00881 standard; protein; 538 AA.

XX AC ABW00881;

XX DT 15-JAN-2004 (first entry)

XX DE Human cytokine receptor, Zalphall protein.

KW Cytokine receptor; Zalphall; cell proliferation; cell development;
 KW splenic disorder; blood disorder; bone disorder; immune disorder;
 KW haematopoietic; lymphoid; inflammatory; therapy; receptor; human.

XX OS Homo sapiens.

XX FH Key Location/Qualifiers

FT Peptide 1..19

FT Protein /label= Signal_peptide

FT Binding-site 20..538

FT Region /note= "Mature human Zalphall protein"

FT Region /note= "Cytokine-binding domain"

FT Region /note= "Domain linker"

FT Domain /note= "Penultimate strand region"

FT Domain /note= "WSXWS motif"

FT Domain /note= "Transmembrane domain"

FT Region /note= "Intracellular signalling domain"

FT Region /note= "Box I signalling site"

FT Region /note= "Box II signalling site"

XX PN US6576744-B1.

XX PD 10-JUN-2003.

XX PF 23-SEP-1999; 99US-00404641.

XX PR 23-SEP-1998; 98US-0100896P.

XX PR 09-MAR-1999; 99US-0123546P.

XX PR 06-JUL-1999; 99US-0142574P.

XX PA (ZYMO) ZYMOGENETICS INC.

XX PI Presnell SR, Conklin DC, Novak JE, Hammond AK;

XX DR WPI; 2003-799829/75.

XX DR N-PSDB; AAD61882.

XX PT Novel cytokine receptor Zalphall useful for treating lymphoid, immune,

XX PT inflammatory, splenic, blood or bone disorders.

XX PS Claim 1; Fig 2; Opp; English.

XX CC The invention relates to a cytokine receptor designated Zalphall and its
 CC nucleic acid sequence. Zalphall protein is useful for detecting ligands
 CC that stimulate the proliferation and/or development of haematopoietic,
 CC lymphoid and myeloid cells in vitro and in vivo. Zalphall DNA is useful
 CC in identifying a region of the genome associated with human disease
 CC states. Zalphall protein is useful for treating lymphoid, immune,
 CC inflammatory, splenic, blood or bone disorders. The present sequence is
 CC human Zalphall protein

XX SQ Sequence 538 AA;

Query Match 100.0%; Score 2958; DB 7; Length 538;
 Best Local Similarity 100.0%; Pred. No. 6.2e-240; Mismatches 0; Indels 0; Gaps 0;
 Matches 538; Conservative 0;

QY 1 MPRGWAAPLLLLLLQGGGCPDLVCYTDYLTQVICILEMNLHPSTLTLTWQDOYEELKD 60
 DB 1 MPRGWAAPLLLLLLQGGGCPDLVCYTDYLTQVICILEMNLHPSTLTLTWQDOYEELKD 60

QY 61 EATCSLHRSAHNATHATYTCMDVHFHMADDIFSVNITDQSGNYSCGCSFLAESIKP 120
 DB 61 EATCSLHRSAHNATHATYTCMDVHFHMADDIFSVNITDQSGNYSCGCSFLAESIKP 120

QY 121 APPFNVTTFSGQYNISWRSDYEDPAFYMLKGKLYELOYRNRGDPWAVSPRKLISVDS 180
 DB 121 APPFNVTTFSGQYNISWRSDYEDPAFYMLKGKLYELOYRNRGDPWAVSPRKLISVDS 180

QY 181 RSVSLLPLEFRKDSSEYELQVRAGPMGSSYQGTWSESDPVIQTQSEELKEGWNPHLLL 240
 DB 181 RSVSLLPLEFRKDSSEYELQVRAGPMGSSYQGTWSESDPVIQTQSEELKEGWNPHLLL 240

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 DB 241 LLLLVIVIFAPWSLKTHPLWRLWKIWAIVSPERFFMPLYKGCSDGFKKWWGAPFTGSS 300

QY 301 LELGWSPEVFTLEVYSCHPPRSPAKRLQLTELQEPALVESDGVPKPSFWPTAQNSSG 360
 DB 301 LELGWSPEVFTLEVYSCHPPRSPAKRLQLTELQEPALVESDGVPKPSFWPTAQNSSG 360

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 DB 361 SAYSEERDRPYGLVSDITVTLDAGPCTWPCSCDDGVPALDLADGLEPSPGLDPLLD 420

QY 421 AGTTVLSGCVSAGSPGLGSLDLRLKPLADGEDWAGGLPWGGRSPGCVSSEAGS 480
 DB 421 AGTTVLSGCVSAGSPGLGSLDLRLKPLADGEDWAGGLPWGGRSPGCVSSEAGS 480

QY 481 FLAGLDMTDFDSGFGVSDCSSPVECDFTSPGDEGPPRSYLRQWVVIPIPLSSPGPQAS 538
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RESULT 15
 ADG87460
 ID ADG87460 standard; protein; 538 AA.
 XX AC ADG87460;
 XX DT 11-MAR-2004 (first entry)
 XX DE Human zalphall protein.
 XX KW zalphall; anaemia; human; gene therapy.
 XX OS Homo sapiens.

XX FH Key Location/Qualifiers
 FT Peptide 1..19
 FT Protein /label= Signal_peptide
 FT Domain /note= "Human mature zalphall protein"
 FT Region /note= "Cytokine binding domain"
 FT Region /note= "Domain linker"
 FT Region /note= "Penultimate strand region"
 FT Domain /note= "Transmembrane domain"
 FT Domain /note= "Complete intracellular signaling domain"
 FT Region /note= "Box I signaling site"
 FT Region /note= "Box II signaling site"

FT /note= "Box II signaling site"
XX US2003148447-A1.
PN
XX 07-AUG-2003.
PD
XX 13-SEP-2002; 2002US-00243072.
XX
XX 28-JUL-2000; 2000US-00628127.
PR
XX (ZYMO) ZYMOGENETICS INC.
PA
XX Presnell SR, Conklin DC, Novak JE, Hammond AK;
PI
XX WPI: 2003-897570/82.
DR N-PSDB; ADG87459.
XX
XX New polynucleotide, useful for preparing a composition for treating e.g.,
PT anemia encodes a zalphall polypeptide cytokine receptor.
PT
XX Claim 1; SEQ ID NO 2; 91pp; English.
PS
XX The present invention relates to new isolated polynucleotide encoding
CC zalphall polypeptide. The polynucleotide is useful for treating anaemia.
CC The invention is useful for producing zalphall polypeptide and producing
CC an antibody to zalphall polypeptide. The present sequence is human
CC zalphall protein.
XX
XX Sequence 538 AA;
SQ
Query Match 100.0%; Score 2958; DB 7; Length 538;
Best Local Similarity 100.0%; Pred. No. 6.2e-240;
Matches 538; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 MPRGWAAPLLLLLGGGCGCDLVCTDYLTQVICILEMWNLHPSTLTWTQDQYEELKD 60
Db 1 MPRGWAAPLLLLLGGGCGCDLVCTDYLTQVICILEMWNLHPSTLTWTQDQYEELKD 60
QY 61 EATCSLHRSANATHATYCHMDVHFHMADDIFSVNITDQSGNYSQCGSFLLAESIKP 120
Db 61 EATCSLHRSANATHATYCHMDVHFHMADDIFSVNITDQSGNYSQCGSFLLAESIKP 120
QY 121 APPFNVTTFSGQYNISWRSYEDPAFYMLKGLQYELQYRNRGDPWAVSPRRKLI SVDS 180
Db 121 APPFNVTTFSGQYNISWRSYEDPAFYMLKGLQYELQYRNRGDPWAVSPRRKLI SVDS 180
QY 181 RVSLLPLEFRKDSSEYELQVRAGMPGSSYQGTWSEWSDPVIPTQSEELKEGWNPHLLL 240
Db 181 RVSLLPLEFRKDSSEYELQVRAGMPGSSYQGTWSEWSDPVIPTQSEELKEGWNPHLLL 240
QY 241 LLLLVIPTPAFWSLTKTHPLWELWKKI WAVSPERFPMPLYKGCSDGFKKWGAPFTGSS 300
Db 241 LLLLVIPTPAFWSLTKTHPLWELWKKI WAVSPERFPMPLYKGCSDGFKKWGAPFTGSS 300
QY 301 LELGWSPEVPSTLEVYSCHPSPRPAKRIQLTEQPAELVESDGVKPKSPFWPTAQNSGG 360
Db 301 LELGWSPEVPSTLEVYSCHPSPRPAKRIQLTEQPAELVESDGVKPKSPFWPTAQNSGG 360
QY 361 SAYSEERDRPYGLVIDTIVLDAEGCTWPCSCDDGYPALDLDAGLEPSPGLEDPDLLD 420
Db 361 SAYSEERDRPYGLVIDTIVLDAEGCTWPCSCDDGYPALDLDAGLEPSPGLEDPDLLD 420
QY 421 AGTTVLSCCVSAGSPGLGGLSLDLRLKPLADGEDWAGGLPWGGRSPGVSESEAGS 480
Db 421 AGTTVLSCCVSAGSPGLGGLSLDLRLKPLADGEDWAGGLPWGGRSPGVSESEAGS 480
QY 481 PLAGLDMDTFDSGFGVSGDCSSPVECDFTSPGDEGPPRSYLRQWVIPPPLSSPGPQAS 538
Db 481 PLAGLDMDTFDSGFGVSGDCSSPVECDFTSPGDEGPPRSYLRQWVIPPPLSSPGPQAS 538

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OM protein - protein search, using sw model

Run on: July 9, 2005, 11:47:11 ; Search time 163 Seconds
(without alignments)
1275.127 Million cell updates/sec

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Perfect score: 2958
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Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1726216 seqs, 386330316 residues

Total number of hits satisfying chosen parameters: 1726216

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Published Applications AA.*

1: /cgn2_6/ptodata/2/pubpaa/US07_PUBCOMB.pep.*
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22: /cgn2_6/ptodata/2/pubpaa/US60_PUBCOMB.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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1	2958	100.0	538	9 US-09-965-313-2	Sequence 2, Appli
2	2958	100.0	538	9 US-09-923-246-115	Sequence 115, App
3	2958	100.0	538	9 US-09-825-561A-2	Sequence 2, Appli
4	2958	100.0	538	10 US-09-972-218A-2	Sequence 2, Appli
5	2958	100.0	538	14 US-10-264-634-2	Sequence 115, App
6	2958	100.0	538	14 US-10-295-723-115	Sequence 115, App
7	2958	100.0	538	14 US-10-282-622-16	Sequence 16, Appli
8	2958	100.0	538	14 US-10-243-072-2	Sequence 2, Appli
9	2958	100.0	538	14 US-10-414-186-2	Sequence 2, Appli
10	2958	100.0	538	15 US-10-456-780-6	Sequence 6, Appli
11	2958	100.0	538	16 US-10-659-684-115	Sequence 115, App

12	2958	100.0	538	16 US-10-620-169-4	Sequence 4, Appli
13	2958	100.0	538	16 US-10-715-998-2	Sequence 2, Appli
14	2958	100.0	538	16 US-10-872-087-2	Sequence 2, Appli
15	2958	100.0	538	16 US-10-787-442-115	Sequence 115, App
16	2958	100.0	538	16 US-10-798-380-43	Sequence 43, Appli
17	2958	100.0	538	17 US-10-864-249-2	Sequence 2, Appli
18	2958	100.0	538	17 US-10-951-239-10	Sequence 10, Appli
19	2951	99.8	538	9 US-09-758-664-2	Sequence 2, Appli
20	2817	95.2	568	9 US-09-758-664-4	Sequence 65, Appli
21	2817	95.2	568	9 US-09-825-561A-65	Sequence 65, Appli
22	2817	95.2	568	9 US-10-872-087-65	Sequence 12, Appli
23	1735.5	58.7	529	9 US-09-825-561A-12	Sequence 10, Appli
24	1735.5	58.7	529	10 US-09-972-218A-10	Sequence 10, Appli
25	1735.5	58.7	529	14 US-10-264-634-10	Sequence 85, Appli
26	1735.5	58.7	529	14 US-10-243-072-85	Sequence 85, Appli
27	1735.5	58.7	529	14 US-10-414-186-85	Sequence 2, Appli
28	1735.5	58.7	529	15 US-10-418-450-2	Sequence 85, Appli
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40	1302	44.0	567	9 US-09-825-561A-16	Sequence 16, Appli
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44	1287	43.5	245	14 US-10-264-634-31	Sequence 25, Appli
45	1287	43.5	467	14 US-10-264-634-25	

ALIGNMENTS

RESULT 1

US-09-965-313-2
; Sequence 2, Application US/09965313
; Patent No. US20020090680A1
; GENERAL INFORMATION:
; APPLICANT: Hodge, Martin R.
; TITLE OF INVENTION: No. US20020090680A1 IL-9/IL-2 Receptor-Like Molecules and Uses Thereof
; FILE REFERENCE: 5800-17A
; CURRENT APPLICATION NUMBER: US/09/965,313
; PRIOR FILING DATE: 2001-09-26
; PRIOR APPLICATION NUMBER: US 09/313,913
; PRIOR FILING DATE: 1999-05-18
; NUMBER OF SEQ ID NOS: 8
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 2
; LENGTH: 538
; TYPE: PRT
; ORGANISM: Homo sapiens IL-2/IL-9 Receptor Like
US-09-965-313-2

Query Match 100.0%; Score 2958; DB 9; Length 538;
Best Local Similarity 100.0%; Pred. No. 2.3e-228;
Matches 538; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY	1	MPRGWAAPLLLLLLQGGWGC	PDLVCYTDYLTQTVICILEMNLHPSTLTLTWDDQYEE	LD 60
DB	1	MPRGWAAPLLLLLLQGGWGC	PDLVCYTDYLTQTVICILEMNLHPSTLTLTWDDQYEE	LD 60
QY	61	EATSCSLHRSAHNATHATYTC	CHMDVFFHPMADDIFSVNITD	SGNSQSCGSLAESIKP 120
DB	61	EATSCSLHRSAHNATHATYTC	CHMDVFFHPMADDIFSVNITD	SGNSQSCGSLAESIKP 120
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481	PLAGLDMDTFDSG	FVSGSPVECDTFS	PGDEGPPRSYL	RQWVVIPPPSSPFGQAS	538
481	PLAGLDMDTFDSG	FVSGSPVECDTFS	PGDEGPPRSYL	RQWVVIPPPSSPFGQAS	538

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RESULT 2
US-09-923-246-115
; Sequence 115, Application US/09923246
; Patent No. US20020128446A1
4 GENERAL INFORMATION:
; APPLICANT: No. US20020128446A1ak, Julia E.
; APPLICANT: Presnell, Scott R.
; APPLICANT: Sprecher, Cindy A.
; APPLICANT: Foster, Donald C.
; APPLICANT: Holly, Richard D.
; APPLICANT: Gross, Jane A.
; APPLICANT: Johnston, Janet V.
; APPLICANT: Nelson, Andrew J.
; APPLICANT: Dillon, Stacey R.
; APPLICANT: Hammond, Angela K.
; TITLE OF INVENTION: NOVEL CYTOKINE ZALPHA11 LIGAND
; FILE REFERENCE: 99-16
; CURRENT APPLICATION NUMBER: US/09/923,246
; CURRENT FILING DATE: 2001-08-03
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: US/09/522,217
; PRIOR FILING DATE: EARLIER FILING DATE: 2000-03-09
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: US 60/123,904
; PRIOR FILING DATE: EARLIER FILING DATE: 1999-03-11
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: US 60/142,013
; PRIOR FILING DATE: EARLIER FILING DATE: 1999-07-01
; NUMBER OF SEQ ID NOS: 115
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 115
; LENGTH: 538
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-923-246-115

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Db	181	RSVSL ¹ PL ² PR ³ K ⁴ OS ⁵ YELQ ⁶ VR ⁷ AG ⁸ MP ⁹ CS ¹⁰ SYQ ¹¹ GT ¹² WS ¹³ WSD ¹⁴ PV ¹⁵ IFOT ¹⁶ SEEL ¹⁷ KEG ¹⁸ WN ¹⁹ PH ²⁰ LL	240
Qy	241	LLL ¹ L ² IV ³ IF ⁴ PA ⁵ F ⁶ W ⁷ SL ⁸ K ⁹ TH ¹⁰ PL ¹¹ W ¹² RL ¹³ WK ¹⁴ IA ¹⁵ VP ¹⁶ SP ¹⁷ ER ¹⁸ FF ¹⁹ MP ²⁰ LY ²¹ K ²² CS ²³ GD ²⁴ FK ²⁵ K ²⁶ W ²⁷ GA ²⁸ PT ²⁹ GS	300
Db	241	LLL ¹ L ² IV ³ IF ⁴ PA ⁵ F ⁶ W ⁷ SL ⁸ K ⁹ TH ¹⁰ PL ¹¹ W ¹² RL ¹³ WK ¹⁴ IA ¹⁵ VP ¹⁶ SP ¹⁷ ER ¹⁸ FF ¹⁹ MP ²⁰ LY ²¹ K ²² CS ²³ GD ²⁴ FK ²⁵ K ²⁶ W ²⁷ GA ²⁸ PT ²⁹ GS	300
Qy	301	LE ¹ GP ² MS ³ PE ⁴ VP ⁵ ST ⁶ LEV ⁷ Y ⁸ S ⁹ CH ¹⁰ PP ¹¹ RS ¹² PA ¹³ K ¹⁴ RL ¹⁵ Q ¹⁶ LB ¹⁷ PA ¹⁸ EL ¹⁹ VE ²⁰ SD ²¹ GP ²² K ²³ PS ²⁴ F ²⁵ WP ²⁶ TA ²⁷ Q ²⁸ NS ²⁹ GG	360
Db	301	LE ¹ GP ² MS ³ PE ⁴ VP ⁵ ST ⁶ LEV ⁷ Y ⁸ S ⁹ CH ¹⁰ PP ¹¹ RS ¹² PA ¹³ K ¹⁴ RL ¹⁵ Q ¹⁶ LB ¹⁷ PA ¹⁸ EL ¹⁹ VE ²⁰ SD ²¹ GP ²² K ²³ PS ²⁴ F ²⁵ WP ²⁶ TA ²⁷ Q ²⁸ NS ²⁹ GG	360
Qy	361	SAY ¹ SEER ² DR ³ Y ⁴ GL ⁵ VS ⁶ ID ⁷ TV ⁸ TL ⁹ DA ¹⁰ B ¹¹ GC ¹² TP ¹³ WC ¹⁴ SC ¹⁵ ED ¹⁶ GY ¹⁷ PAL ¹⁸ DL ¹⁹ DAG ²⁰ LE ²¹ PS ²² GC ²³ LE ²⁴ PL ²⁵ LD	420
Db	361	SAY ¹ SEER ² DR ³ Y ⁴ GL ⁵ VS ⁶ ID ⁷ TV ⁸ TL ⁹ DA ¹⁰ B ¹¹ GC ¹² TP ¹³ WC ¹⁴ SC ¹⁵ ED ¹⁶ GY ¹⁷ PAL ¹⁸ DL ¹⁹ DAG ²⁰ LE ²¹ PS ²² GC ²³ LE ²⁴ PL ²⁵ LD	420
Qy	421	AG ¹ TV ² LC ³ GC ⁴ VS ⁵ AG ⁶ SP ⁷ GL ⁸ GG ⁹ PL ¹⁰ GS ¹¹ LD ¹² RL ¹³ K ¹⁴ PL ¹⁵ AD ¹⁶ GED ¹⁷ WAG ¹⁸ GL ¹⁹ PW ²⁰ GR ²¹ SP ²² GG ²³ YSE ²⁴ AG ²⁵ S	480
Db	421	AG ¹ TV ² LC ³ GC ⁴ VS ⁵ AG ⁶ SP ⁷ GL ⁸ GG ⁹ PL ¹⁰ GS ¹¹ LD ¹² RL ¹³ K ¹⁴ PL ¹⁵ AD ¹⁶ GED ¹⁷ WAG ¹⁸ GL ¹⁹ PW ²⁰ GR ²¹ SP ²² GG ²³ YSE ²⁴ AG ²⁵ S	480
Qy	481	PL ¹ AG ² LD ³ MD ⁴ T ⁵ FD ⁶ SG ⁷ VG ⁸ SD ⁹ CS ¹⁰ SP ¹¹ VE ¹² CD ¹³ FT ¹⁴ SP ¹⁵ GD ¹⁶ SG ¹⁷ PP ¹⁸ RY ¹⁹ L ²⁰ RQ ²¹ W ²² V ²³ IP ²⁴ PL ²⁵ SS ²⁶ PG ²⁷ QO ²⁸ AS	538
Db	481	PL ¹ AG ² LD ³ MD ⁴ T ⁵ FD ⁶ SG ⁷ VG ⁸ SD ⁹ CS ¹⁰ SP ¹¹ VE ¹² CD ¹³ FT ¹⁴ SP ¹⁵ GD ¹⁶ SG ¹⁷ PP ¹⁸ RY ¹⁹ L ²⁰ RQ ²¹ W ²² V ²³ IP ²⁴ PL ²⁵ SS ²⁶ PG ²⁷ QO ²⁸ AS	538

```

RESULT 3
US-09-825-561A-2
; Sequence 2, Application US/09825561A
; Patent No. US2002013767A1
; GENERAL INFORMATION:
; APPLICANT: Sprecher, Cindy A.
; APPLICANT: No. US20020137677Alak, Julia E.
; APPLICANT: West, James W.
; APPLICANT: Presnell, Scott R.
; APPLICANT: Holly, Richard D.
; APPLICANT: Nelson, Andrew J.
; TITLE OF INVENTION: SOLUBLE ZALPHA11 CYTOKINE RECEPTORS
; FILE REFERENCE: 00-22
; CURRENT APPLICATION NUMBER: US/09/825,561A
; CURRENT FILING DATE: 2000-04-05
; PRIOR APPLICATION NUMBER: US 60/194,731
; PRIOR FILING DATE: 2000-04-05
; PRIOR APPLICATION NUMBER: US 60/222,121
; PRIOR FILING DATE: 2000-07-28
; NUMBER OF SEQ ID NOS: 86
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 2
; LENGTH: 538
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-825-561A-2

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[illegible]


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Db 181 RVSLLPLEFRKDSSEYELQVRAGMPGSSYQGTWSESDPVIPTQSEBELKEGWNPHLLL 240
Qy 241 LLLLVIPIPAFWSLKTHPLRLWKKIWAVSPERFFMPLYKGCSDGDFKWKWGAPFTGSS 300
Db 241 LLLLVIPIPAFWSLKTHPLRLWKKIWAVSPERFFMPLYKGCSDGDFKWKWGAPFTGSS 300
Qy 301 LELGWSPEVPSTLEVISCHPPRSPAKRLQLTELQEPABELVSDGVKPSFWPTAQNSGG 360
Db 301 LELGWSPEVPSTLEVISCHPPRSPAKRLQLTELQEPABELVSDGVKPSFWPTAQNSGG 360
Qy 361 SAYSEERDRPYGLVSTDTVTVLDAEGPCTWPCSCDDGYPALDLADGLEPSPGLEDPDLLD 420
Db 361 SAYSEERDRPYGLVSTDTVTVLDAEGPCTWPCSCDDGYPALDLADGLEPSPGLEDPDLLD 420
Qy 421 AGTTVLSCGCVSAGSAGPLGGLSLDLRLKPLADGEDWAGGLPWGGRSPGGVSSEAGS 480
Db 421 AGTTVLSCGCVSAGSAGPLGGLSLDLRLKPLADGEDWAGGLPWGGRSPGGVSSEAGS 480
Qy 481 PLAGLDMDTFDSGFGVSDCSPVECDFTSPGDEGPPRSYLROWVIPPPLSSPGPQAS 538
Db 481 PLAGLDMDTFDSGFGVSDCSPVECDFTSPGDEGPPRSYLROWVIPPPLSSPGPQAS 538
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RESULT 4

US-09-972-218A-2

; Sequence 2, Application US/09972218A

; Publication No. US20030049798A1

; GENERAL INFORMATION:

; APPLICANT: Carter, Laura

; APPLICANT: Whitters, Matthew J

; APPLICANT: Collins, Mary

; APPLICANT: Young, Deborah A.

; APPLICANT: Donaldson, Debra D.

; APPLICANT: Lowe, Leslie D.

; APPLICANT: Unger, Michelle

; TITLE OF INVENTION: MU-1, Member of the Cytokine Receptor Family

; FILE REFERENCE: 22058-552CIP2

; CURRENT APPLICATION NUMBER: US/09/972,218A

; CURRENT FILING DATE: 2002-08-19

; PRIOR APPLICATION NUMBER: 09/569384

; PRIOR FILING DATE: 2000-05-11

; PRIOR APPLICATION NUMBER: 09/560766

; PRIOR FILING DATE: 2000-04-28

; PRIOR APPLICATION NUMBER: US/6057128

; PRIOR FILING DATE: 1998-03-17

; NUMBER OF SEQ ID NOS: 21

; SOFTWARE: Patent In Ver. 2.1

; SEQ ID NO 2

; LENGTH: 538

; TYPE: PRT

; ORGANISM: Human

US-09-972-218A-2

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Query Match 100.0%; Score 2958; DB 10; Length 538;
Best Local Similarity 100.0%; Pred. No. 2.3e-228;
Matches 538; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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Qy 1 MPRGWAAPLLLLLLLOGGWCPCDPLVCYTDYLTQTVICILEMNNLHPSTLTLTWQDOYEELKD 60
Db 1 MPRGWAAPLLLLLLLOGGWCPCDPLVCYTDYLTQTVICILEMNNLHPSTLTLTWQDOYEELKD 60
Qy 61 EATCSLHRSNAHNAHTATYCHMDVHFHMADDIFSVNITDQSGNYSQECGSFLLAESIKP 120
Db 61 EATCSLHRSNAHNAHTATYCHMDVHFHMADDIFSVNITDQSGNYSQECGSFLLAESIKP 120
Qy 121 APPFNVTTFSGQYNISWRSYEDPAFYMLKGLQYELQYRNRPDPAWSPRRKLISVDS 180
Db 121 APPFNVTTFSGQYNISWRSYEDPAFYMLKGLQYELQYRNRPDPAWSPRRKLISVDS 180
Qy 181 RVSLLPLEFRKDSSEYELQVRAGMPGSSYQGTWSESDPVIPTQSEBELKEGWNPHLLL 240
Db 181 RVSLLPLEFRKDSSEYELQVRAGMPGSSYQGTWSESDPVIPTQSEBELKEGWNPHLLL 240
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Qy 241 LLLLVIPIPAFWSLKTHPLRLWKKIWAVSPERFFMPLYKGCSDGDFKWKWGAPFTGSS 300
Db 241 LLLLVIPIPAFWSLKTHPLRLWKKIWAVSPERFFMPLYKGCSDGDFKWKWGAPFTGSS 300
Qy 301 LELGWSPEVPSTLEVISCHPPRSPAKRLQLTELQEPABELVSDGVKPSFWPTAQNSGG 360
Db 301 LELGWSPEVPSTLEVISCHPPRSPAKRLQLTELQEPABELVSDGVKPSFWPTAQNSGG 360
Qy 361 SAYSEERDRPYGLVSTDTVTVLDAEGPCTWPCSCDDGYPALDLADGLEPSPGLEDPDLLD 420
Db 361 SAYSEERDRPYGLVSTDTVTVLDAEGPCTWPCSCDDGYPALDLADGLEPSPGLEDPDLLD 420
Qy 421 AGTTVLSCGCVSAGSAGPLGGLSLDLRLKPLADGEDWAGGLPWGGRSPGGVSSEAGS 480
Db 421 AGTTVLSCGCVSAGSAGPLGGLSLDLRLKPLADGEDWAGGLPWGGRSPGGVSSEAGS 480
Qy 481 PLAGLDMDTFDSGFGVSDCSPVECDFTSPGDEGPPRSYLROWVIPPPLSSPGPQAS 538
Db 481 PLAGLDMDTFDSGFGVSDCSPVECDFTSPGDEGPPRSYLROWVIPPPLSSPGPQAS 538
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RESULT 5

US-10-264-634-2

; Sequence 2, Application US/10264634

; Publication No. US20030108549A1

; GENERAL INFORMATION:

; APPLICANT: Donaldson, Debra et al.

; TITLE OF INVENTION: Methods and Compositions for Modulating Interleukin-21 Receptor

; FILE REFERENCE: G15320-P3

; CURRENT APPLICATION NUMBER: US/10/264,634

; CURRENT FILING DATE: 2002-10-04

; PRIOR APPLICATION NUMBER: 09/040,005

; PRIOR FILING DATE: 1998-03-17

; PRIOR APPLICATION NUMBER: 09/560,766

; PRIOR FILING DATE: 2000-04-28

; PRIOR APPLICATION NUMBER: 09/569,384

; PRIOR FILING DATE: 2000-05-11

; PRIOR APPLICATION NUMBER: 09/972,218

; PRIOR FILING DATE: 2001-10-04

; PRIOR APPLICATION NUMBER: 60/373,746

; PRIOR FILING DATE: 2002-04-17

; NUMBER OF SEQ ID NOS: 44

; SOFTWARE: Patent in version 3.1

; SEQ ID NO 2

; LENGTH: 538

; TYPE: PRT

; ORGANISM: Human

US-10-264-634-2

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Query Match 100.0%; Score 2958; DB 14; Length 538;
Best Local Similarity 100.0%; Pred. No. 2.3e-228;
Matches 538; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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Qy 1 MPRGWAAPLLLLLLLOGGWCPCDPLVCYTDYLTQTVICILEMNNLHPSTLTLTWQDOYEELKD 60
Db 1 MPRGWAAPLLLLLLLOGGWCPCDPLVCYTDYLTQTVICILEMNNLHPSTLTLTWQDOYEELKD 60
Qy 61 EATCSLHRSNAHNAHTATYCHMDVHFHMADDIFSVNITDQSGNYSQECGSFLLAESIKP 120
Db 61 EATCSLHRSNAHNAHTATYCHMDVHFHMADDIFSVNITDQSGNYSQECGSFLLAESIKP 120
Qy 121 APPFNVTTFSGQYNISWRSYEDPAFYMLKGLQYELQYRNRPDPAWSPRRKLISVDS 180
Db 121 APPFNVTTFSGQYNISWRSYEDPAFYMLKGLQYELQYRNRPDPAWSPRRKLISVDS 180
Qy 181 RVSLLPLEFRKDSSEYELQVRAGMPGSSYQGTWSESDPVIPTQSEBELKEGWNPHLLL 240
Db 181 RVSLLPLEFRKDSSEYELQVRAGMPGSSYQGTWSESDPVIPTQSEBELKEGWNPHLLL 240
Qy 241 LLLLVIPIPAFWSLKTHPLRLWKKIWAVSPERFFMPLYKGCSDGDFKWKWGAPFTGSS 300
Db 241 LLLLVIPIPAFWSLKTHPLRLWKKIWAVSPERFFMPLYKGCSDGDFKWKWGAPFTGSS 300
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Qy 301 LELGWSPEVPSTLEVSCHPPSPAKRLQTLQEPALVESDGVKPSFWPTAQNSSG 360
Db |||||
301 LELGWSPEVPSTLEVSCHPPSPAKRLQTLQEPALVESDGVKPSFWPTAQNSSG 360
Qy 361 SAYSEERDRPYGLVSIIDTVTLDAEGCTWPCSCDDGYPALDLDAGLEPSGLDPLLD 420
Db |||||
361 SAYSEERDRPYGLVSIIDTVTLDAEGCTWPCSCDDGYPALDLDAGLEPSGLDPLLD 420
Qy 421 AGTTVLSGCVSAGSPGLGGLSLDLRLKPLADGEDWAGGLPWGSRPGVSESEAGS 480
Db |||||
421 AGTTVLSGCVSAGSPGLGGLSLDLRLKPLADGEDWAGGLPWGSRPGVSESEAGS 480
Qy 481 PLAGLDMTDFSGFVSGDCSPVECDFTSPGDEGPPRSYLRQWVVIPTPLSSPGPOAS 538
Db |||||
481 PLAGLDMTDFSGFVSGDCSPVECDFTSPGDEGPPRSYLRQWVVIPTPLSSPGPOAS 538

RESULT 6

US-10-295-723-115
; Sequence 115, Application US/10295723
; Publication No. US20030125524A1
; GENERAL INFORMATION:
; APPLICANT: No. US20030125524A1ak, Julia E.
; APPLICANT: Presnell, Scott R.
; APPLICANT: Sprecher, Cindy A.
; APPLICANT: Foster, Donald C.
; APPLICANT: Holly, Richard D.
; APPLICANT: Gross, Jane A.
; APPLICANT: Johnston, Janet V.
; APPLICANT: Nelson, Andrew J.
; APPLICANT: Dillon, Stacey R.
; APPLICANT: Hammond, Angela K.
; TITLE OF INVENTION: NOVEL CYTOKINE ZALPHA11 LIGAND
; FILE REFERENCE: 99-16
; CURRENT APPLICATION NUMBER: US/10/295,723
; CURRENT FILING DATE: 2002-11-15
; PRIOR APPLICATION NUMBER: 09/522,217
; PRIOR FILING DATE: 2000-03-09
; PRIOR APPLICATION NUMBER: US 60/123,547
; PRIOR FILING DATE: 1999-03-09
; PRIOR APPLICATION NUMBER: US 60/123,904
; PRIOR FILING DATE: 1999-03-11
; PRIOR APPLICATION NUMBER: US 60/142,013
; PRIOR FILING DATE: 1999-07-01
; NUMBER OF SEQ ID NOS: 115
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 115
; LENGTH: 538
; TYPE: PRT
; ORGANISM: Homo sapiens

US-10-295-723-115

Query Match 100.0%; Score 2958; DB 14; Length 538;
Best Local Similarity 100.0%; Pred. No. 2.3e-228;
Matches 538; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 MPRGWAAPLLLLLQGGWGCPLVCYTDYLTQTVICILEMNLHPSTLTLTWQDQYEELKD 60
Db |||||
1 MPRGWAAPLLLLLQGGWGCPLVCYTDYLTQTVICILEMNLHPSTLTLTWQDQYEELKD 60
Qy 61 EATCSLHRSAHNATHATYTCMDVHFHMADDIFSVNITDQSGNYSQCGSFLLAESIKP 120
Db |||||
61 EATCSLHRSAHNATHATYTCMDVHFHMADDIFSVNITDQSGNYSQCGSFLLAESIKP 120
Qy 121 APPFNVTTFSGQYNISWRSDYEDPAFYMLKGKQLQYELQYLRNRPDPAVSPRRKLIISVDS 180
Db |||||
121 APPFNVTTFSGQYNISWRSDYEDPAFYMLKGKQLQYELQYLRNRPDPAVSPRRKLIISVDS 180
Qy 181 RSVSLLPLEFRKDSSEYELQVRAGMPGSSYOGTWSEWSDPVIQTQSEELKEGWNPHLLL 240
Db |||||
181 RSVSLLPLEFRKDSSEYELQVRAGMPGSSYOGTWSEWSDPVIQTQSEELKEGWNPHLLL 240
Qy 240 LELGWSPEVPSTLEVSCHPPSPAKRLQTLQEPALVESDGVKPSFWPTAQNSSG 360
Db |||||
240 LELGWSPEVPSTLEVSCHPPSPAKRLQTLQEPALVESDGVKPSFWPTAQNSSG 360
Qy 360 LELGWSPEVPSTLEVSCHPPSPAKRLQTLQEPALVESDGVKPSFWPTAQNSSG 360
Db |||||
360 LELGWSPEVPSTLEVSCHPPSPAKRLQTLQEPALVESDGVKPSFWPTAQNSSG 360

Qy 241 LLLLVIVIFIPAFWSLKTPLWLWKKIWAVPSPERFFMPLYKGCSDGFKWVGAPFTGSS 300
Db |||||
241 LLLLVIVIFIPAFWSLKTPLWLWKKIWAVPSPERFFMPLYKGCSDGFKWVGAPFTGSS 300
Qy 301 LELGWSPEVPSTLEVSCHPPSPAKRLQTLQEPALVESDGVKPSFWPTAQNSSG 360
Db |||||
301 LELGWSPEVPSTLEVSCHPPSPAKRLQTLQEPALVESDGVKPSFWPTAQNSSG 360
Qy 361 SAYSEERDRPYGLVSIIDTVTLDAEGCTWPCSCDDGYPALDLDAGLEPSGLDPLLD 420
Db |||||
361 SAYSEERDRPYGLVSIIDTVTLDAEGCTWPCSCDDGYPALDLDAGLEPSGLDPLLD 420
Qy 421 AGTTVLSGCVSAGSPGLGGLSLDLRLKPLADGEDWAGGLPWGSRPGVSESEAGS 480
Db |||||
421 AGTTVLSGCVSAGSPGLGGLSLDLRLKPLADGEDWAGGLPWGSRPGVSESEAGS 480
Qy 481 PLAGLDMTDFSGFVSGDCSPVECDFTSPGDEGPPRSYLRQWVVIPTPLSSPGPOAS 538
Db |||||
481 PLAGLDMTDFSGFVSGDCSPVECDFTSPGDEGPPRSYLRQWVVIPTPLSSPGPOAS 538

RESULT 7

US-10-282-622-16
; Sequence 16, Application US/10282622
; Publication No. US20030134390A1
; GENERAL INFORMATION:
; APPLICANT: Presnell, Scott R.
; APPLICANT: West, James W.
; APPLICANT: No. US20030134390A1ak, Julia E.
; TITLE OF INVENTION: ZALPHA11 LIGAND ANTAGONISTS
; FILE REFERENCE: 01-37
; CURRENT APPLICATION NUMBER: US/10/282,622
; CURRENT FILING DATE: 2002-10-28
; PRIOR APPLICATION NUMBER: 60/337,586
; PRIOR FILING DATE: 2001-11-05
; NUMBER OF SEQ ID NOS: 30
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 16
; LENGTH: 538
; TYPE: PRT
; ORGANISM: Homo sapiens

US-10-282-622-16

Query Match 100.0%; Score 2958; DB 14; Length 538;
Best Local Similarity 100.0%; Pred. No. 2.3e-228;
Matches 538; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 MPRGWAAPLLLLLQGGWGCPLVCYTDYLTQTVICILEMNLHPSTLTLTWQDQYEELKD 60
Db |||||
1 MPRGWAAPLLLLLQGGWGCPLVCYTDYLTQTVICILEMNLHPSTLTLTWQDQYEELKD 60
Qy 61 EATCSLHRSAHNATHATYTCMDVHFHMADDIFSVNITDQSGNYSQCGSFLLAESIKP 120
Db |||||
61 EATCSLHRSAHNATHATYTCMDVHFHMADDIFSVNITDQSGNYSQCGSFLLAESIKP 120
Qy 121 APPFNVTTFSGQYNISWRSDYEDPAFYMLKGKQLQYELQYLRNRPDPAVSPRRKLIISVDS 180
Db |||||
121 APPFNVTTFSGQYNISWRSDYEDPAFYMLKGKQLQYELQYLRNRPDPAVSPRRKLIISVDS 180
Qy 181 RSVSLLPLEFRKDSSEYELQVRAGMPGSSYOGTWSEWSDPVIQTQSEELKEGWNPHLLL 240
Db |||||
181 RSVSLLPLEFRKDSSEYELQVRAGMPGSSYOGTWSEWSDPVIQTQSEELKEGWNPHLLL 240
Qy 241 LLLLVIVIFIPAFWSLKTPLWLWKKIWAVPSPERFFMPLYKGCSDGFKWVGAPFTGSS 300
Db |||||
241 LLLLVIVIFIPAFWSLKTPLWLWKKIWAVPSPERFFMPLYKGCSDGFKWVGAPFTGSS 300
Qy 301 LELGWSPEVPSTLEVSCHPPSPAKRLQTLQEPALVESDGVKPSFWPTAQNSSG 360
Db |||||
301 LELGWSPEVPSTLEVSCHPPSPAKRLQTLQEPALVESDGVKPSFWPTAQNSSG 360
Qy 361 SAYSEERDRPYGLVSIIDTVTLDAEGCTWPCSCDDGYPALDLDAGLEPSGLDPLLD 420
Db |||||
361 SAYSEERDRPYGLVSIIDTVTLDAEGCTWPCSCDDGYPALDLDAGLEPSGLDPLLD 420

Db 361 SAYSEDRPYGLVSDITVTVLDAEGCTWPCSCDDGYPALDLDAGLEPSPGLEDPDLD 420
Qy 421 AGTTVLSGCCVSAAGSGLGGPLGSLDLRLKPLADGEDWAGGLPWGGRSPGVSSSEAGS 480
Db 421 AGTTVLSGCCVSAAGSGLGGPLGSLDLRLKPLADGEDWAGGLPWGGRSPGVSSSEAGS 480
Qy 481 PLAGLMDMTFDSGFVSGDCSSPVECDFTSPGDEGPRSYLRQWVITPPPLSSPGPOAS 538
Db 481 PLAGLMDMTFDSGFVSGDCSSPVECDFTSPGDEGPRSYLRQWVITPPPLSSPGPOAS 538

RESULT 8

US-10-243-072-2
; Sequence 2, Application US/10243072
; Publication No. US2003014847A1
; GENERAL INFORMATION:
; APPLICANT: Presnell, Scott R.
; APPLICANT: Conklin, Darrell C.
; APPLICANT: No. US2003014847A1ak, Julia E.
; APPLICANT: Hammond, Angela K.
; TITLE OF INVENTION: CYTOKINE RECEPTOR ZAPLHALL
; FILE REFERENCE: 98-55C1
; CURRENT APPLICATION NUMBER: US/10/243,072
; PRIOR FILING DATE: 2002-09-13
; PRIOR APPLICATION NUMBER: 09/628,127
; PRIOR FILING DATE: 2000-07-28
; PRIOR APPLICATION NUMBER: US 60/100,896
; PRIOR FILING DATE: 1998-09-23
; PRIOR APPLICATION NUMBER: US 60/123,546
; PRIOR FILING DATE: 1999-03-09
; PRIOR APPLICATION NUMBER: US 60/142,574
; PRIOR FILING DATE: 1999-07-06
; PRIOR APPLICATION NUMBER: US 09/404,641
; PRIOR FILING DATE: 1999-09-23
; NUMBER OF SEQ ID NOS: 92
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 2
; LENGTH: 538
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-243-072-2

Query Match 100.0%; Score 2958; DB 14; Length 538;
Best Local Similarity 100.0%; Pred. No. 2.3e-228;
Matches 538; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 MPRGWAAPLLLLLLQGGWGPCDLCVCTDYLTQVTCILEMNNLHPSTLTLTWQDQYEELKD 60
Db 1 MPRGWAAPLLLLLLQGGWGPCDLCVCTDYLTQVTCILEMNNLHPSTLTLTWQDQYEELKD 60
Qy 61 EATCSLHRSNAHNAHTATYTCMDVHFHMAADDIFSVNITDQSGNYSQECGSPFLAESIKP 120
Db 61 EATCSLHRSNAHNAHTATYTCMDVHFHMAADDIFSVNITDQSGNYSQECGSPFLAESIKP 120
Qy 121 APPFNVTTFSGQYNISWRSDYEDPAFYMKGKQYELQYRNRGDPWAVSPRRKLISVDS 180
Db 121 APPFNVTTFSGQYNISWRSDYEDPAFYMKGKQYELQYRNRGDPWAVSPRRKLISVDS 180
Qy 181 RSVSLLPLEFRKDSYELQVRAGMPGSSYQGTWSESDPVIQTQSEBELKEGWNPHLL 240
Db 181 RSVSLLPLEFRKDSYELQVRAGMPGSSYQGTWSESDPVIQTQSEBELKEGWNPHLL 240
Qy 241 LLLLVIPIPAFWSLKTPLRLWKKIWAVSPERFPMPLKGCSDGFKKWGAPFTGSS 300
Db 241 LLLLVIPIPAFWSLKTPLRLWKKIWAVSPERFPMPLKGCSDGFKKWGAPFTGSS 300
Qy 301 LELGWSPEVSTLEVISCHPPRSPAKRLQLTELQEPALVESDGVKPKSPFWPTAQNCGG 360
Db 301 LELGWSPEVSTLEVISCHPPRSPAKRLQLTELQEPALVESDGVKPKSPFWPTAQNCGG 360
Qy 361 SAYSEDRPYGLVSDITVTVLDAEGCTWPCSCDDGYPALDLDAGLEPSPGLEDPDLD 420
Db 361 SAYSEDRPYGLVSDITVTVLDAEGCTWPCSCDDGYPALDLDAGLEPSPGLEDPDLD 420

RESULT 9

US-10-414-186-2
; Sequence 2, Application US/10414186
; Publication No. US20030175825A1
; GENERAL INFORMATION:
; APPLICANT: Presnell, Scott R.
; APPLICANT: Conklin, Darrell C.
; APPLICANT: No. US20030175825A1ak, Julia E.
; APPLICANT: Hammond, Angela K.
; TITLE OF INVENTION: CYTOKINE RECEPTOR ZAPLHALL
; FILE REFERENCE: 98-55
; CURRENT APPLICATION NUMBER: US/10/414,186
; CURRENT FILING DATE: 2003-04-14
; PRIOR APPLICATION NUMBER: US/09/404,641
; PRIOR FILING DATE: 1999-09-23
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: US 60/100,896
; PRIOR FILING DATE: EARLIER FILING DATE: 1998-09-23
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: US 60/123,546
; PRIOR FILING DATE: EARLIER FILING DATE: 1999-03-09
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: US 60/142,574
; PRIOR FILING DATE: EARLIER FILING DATE: 1999-07-06
; NUMBER OF SEQ ID NOS: 91
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 2
; LENGTH: 538
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-414-186-2

Query Match 100.0%; Score 2958; DB 14; Length 538;
Best Local Similarity 100.0%; Pred. No. 2.3e-228;
Matches 538; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 MPRGWAAPLLLLLLQGGWGPCDLCVCTDYLTQVTCILEMNNLHPSTLTLTWQDQYEELKD 60
Db 1 MPRGWAAPLLLLLLQGGWGPCDLCVCTDYLTQVTCILEMNNLHPSTLTLTWQDQYEELKD 60
Qy 61 EATCSLHRSNAHNAHTATYTCMDVHFHMAADDIFSVNITDQSGNYSQECGSPFLAESIKP 120
Db 61 EATCSLHRSNAHNAHTATYTCMDVHFHMAADDIFSVNITDQSGNYSQECGSPFLAESIKP 120
Qy 121 APPFNVTTFSGQYNISWRSDYEDPAFYMKGKQYELQYRNRGDPWAVSPRRKLISVDS 180
Db 121 APPFNVTTFSGQYNISWRSDYEDPAFYMKGKQYELQYRNRGDPWAVSPRRKLISVDS 180
Qy 181 RSVSLLPLEFRKDSYELQVRAGMPGSSYQGTWSESDPVIQTQSEBELKEGWNPHLL 240
Db 181 RSVSLLPLEFRKDSYELQVRAGMPGSSYQGTWSESDPVIQTQSEBELKEGWNPHLL 240
Qy 241 LLLLVIPIPAFWSLKTPLRLWKKIWAVSPERFPMPLKGCSDGFKKWGAPFTGSS 300
Db 241 LLLLVIPIPAFWSLKTPLRLWKKIWAVSPERFPMPLKGCSDGFKKWGAPFTGSS 300
Qy 301 LELGWSPEVSTLEVISCHPPRSPAKRLQLTELQEPALVESDGVKPKSPFWPTAQNCGG 360
Db 301 LELGWSPEVSTLEVISCHPPRSPAKRLQLTELQEPALVESDGVKPKSPFWPTAQNCGG 360
Qy 361 SAYSEDRPYGLVSDITVTVLDAEGCTWPCSCDDGYPALDLDAGLEPSPGLEDPDLD 420
Db 361 SAYSEDRPYGLVSDITVTVLDAEGCTWPCSCDDGYPALDLDAGLEPSPGLEDPDLD 420
Qy 421 AGTTVLSGCCVSAAGSGLGGPLGSLDLRLKPLADGEDWAGGLPWGGRSPGVSSSEAGS 480

Db 421 AGTTVLSCGCVSAGSPGLGGLSLDLRLKPLADGEDWAGLPGWGRSPGCVSESEAGS 480
QY 481 PLAGLDMDTDSGFGVSDCSPEVCDFTSPGDEGPPRSYLRQWVVIPTLSSPGPQAS 538
Db 481 PLAGLDMDTDSGFGVSDCSPEVCDFTSPGDEGPPRSYLRQWVVIPTLSSPGPQAS 538

RESULT 10
US-10-456-780-6
; Sequence 6, Application US/10456780
; Publication No. US20040009150A1
; GENERAL INFORMATION:
; APPLICANT: Nelson, Andrew J.
; APPLICANT: Hughes, Steven D.
; APPLICANT: Holly, Richard D.
; TITLE OF INVENTION: USE OF IL-21 IN CANCER AND
; TITLE OF INVENTION: OTHER THERAPEUTIC APPLICATIONS
; FILE REFERENCE: 03-08
; CURRENT APPLICATION NUMBER: US/10/456,780
; PRIOR FILING DATE: 2003-06-06
; PRIOR APPLICATION NUMBER: US 60/387,127
; PRIOR FILING DATE: 2002-06-07
; NUMBER OF SEQ ID NOS: 17
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 6
; LENGTH: 538
; TYPE: PRT
; ORGANISM: Homo sapiens
; US-10-456-780-6

Query Match 100.0%; Score 2958; DB 15; Length 538;
Best Local Similarity 100.0%; Pred. No. 2.3e-228;
Matches 538; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MPRGWAAPLLLLLQGGWCPDLVCYTDYLTQTVICILEMNNLHPSTLTLTWQDQYEELKD 60
Db 1 MPRGWAAPLLLLLQGGWCPDLVCYTDYLTQTVICILEMNNLHPSTLTLTWQDQYEELKD 60
QY 61 EATCSLHRSAHNATHATYTCCHMDVHFHMADDIFSVNITDQSGYSCGCSFLAESTKP 120
Db 61 EATCSLHRSAHNATHATYTCCHMDVHFHMADDIFSVNITDQSGYSCGCSFLAESTKP 120
QY 121 APPFNVTTFSGQYNISRSYEDPAFYMLKGKQLQYELQYRNRGDPMVSPRRKLIISVDS 180
Db 121 APPFNVTTFSGQYNISRSYEDPAFYMLKGKQLQYELQYRNRGDPMVSPRRKLIISVDS 180
QY 181 RSVSLLPLEFRKDSYELQVRAGMPGSSYQGTWSESDPVI FQTQSEELKEGWNPHLLL 240
Db 181 RSVSLLPLEFRKDSYELQVRAGMPGSSYQGTWSESDPVI FQTQSEELKEGWNPHLLL 240
QY 241 LLLLVIVFIPAFWSLTKTHPLWRLWKIWA VSPERFPMPLYKGCSDGDFKRWGAPFTGSS 300
Db 241 LLLLVIVFIPAFWSLTKTHPLWRLWKIWA VSPERFPMPLYKGCSDGDFKRWGAPFTGSS 300
QY 301 LELGWPSPVSTLEVYSCHPSPRPAKRLQLTQLQEPALVESDGVKPSFWPTAQNSSG 360
Db 301 LELGWPSPVSTLEVYSCHPSPRPAKRLQLTQLQEPALVESDGVKPSFWPTAQNSSG 360
QY 361 SAYSEERDRPYGLVSIIDTVTLDAEGPCTWPCSCDDGYPALDLADGLESPGLEDPILLD 420
Db 361 SAYSEERDRPYGLVSIIDTVTLDAEGPCTWPCSCDDGYPALDLADGLESPGLEDPILLD 420
QY 421 AGTTVLSCGCVSAGSPGLGGLSLDLRLKPLADGEDWAGLPGWGRSPGCVSESEAGS 480
Db 421 AGTTVLSCGCVSAGSPGLGGLSLDLRLKPLADGEDWAGLPGWGRSPGCVSESEAGS 480
QY 481 PLAGLDMDTDSGFGVSDCSPEVCDFTSPGDEGPPRSYLRQWVVIPTLSSPGPQAS 538
Db 481 PLAGLDMDTDSGFGVSDCSPEVCDFTSPGDEGPPRSYLRQWVVIPTLSSPGPQAS 538

RESULT 11
US-10-659-684-115

; Sequence 115, Application US/10659684
; Publication No. US20040110932A1
; GENERAL INFORMATION:
; APPLICANT: Novak, Julia E.
; APPLICANT: Presnell, Scott R.
; APPLICANT: Sprecher, Cindy A.
; APPLICANT: Foster, Donald C.
; APPLICANT: Holly, Richard D.
; APPLICANT: Gross, Jane A.
; APPLICANT: Johnston, Janet V.
; APPLICANT: Nelson, Andrew J.
; APPLICANT: Dillon, Stacey R.
; APPLICANT: Hammond, Angela K.
; TITLE OF INVENTION: NOVEL CYTOKINE ZALPHA11 LIGAND
; FILE REFERENCE: 99-16
; CURRENT APPLICATION NUMBER: US/10/659,684
; CURRENT FILING DATE: 2003-09-10
; PRIOR APPLICATION NUMBER: US/09/522,217
; PRIOR FILING DATE: 2000-03-09
; PRIOR APPLICATION NUMBER: EARLIER FILING DATE: 1999-03-09
; PRIOR FILING DATE: EARLIER FILING DATE: 1999-03-09
; PRIOR APPLICATION NUMBER: EARLIER FILING DATE: 1999-03-11
; PRIOR FILING DATE: EARLIER FILING DATE: 1999-03-11
; PRIOR APPLICATION NUMBER: EARLIER FILING DATE: 1999-07-01
; PRIOR FILING DATE: EARLIER FILING DATE: 1999-07-01
; NUMBER OF SEQ ID NOS: 115
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 115
; LENGTH: 538
; TYPE: PRT
; ORGANISM: Homo sapiens
; US-10-659-684-115

Query Match 100.0%; Score 2958; DB 16; Length 538;
Best Local Similarity 100.0%; Pred. No. 2.3e-228;
Matches 538; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MPRGWAAPLLLLLQGGWCPDLVCYTDYLTQTVICILEMNNLHPSTLTLTWQDQYEELKD 60
Db 1 MPRGWAAPLLLLLQGGWCPDLVCYTDYLTQTVICILEMNNLHPSTLTLTWQDQYEELKD 60
QY 61 EATCSLHRSAHNATHATYTCCHMDVHFHMADDIFSVNITDQSGYSCGCSFLAESTKP 120
Db 61 EATCSLHRSAHNATHATYTCCHMDVHFHMADDIFSVNITDQSGYSCGCSFLAESTKP 120
QY 121 APPFNVTTFSGQYNISRSYEDPAFYMLKGKQLQYELQYRNRGDPMVSPRRKLIISVDS 180
Db 121 APPFNVTTFSGQYNISRSYEDPAFYMLKGKQLQYELQYRNRGDPMVSPRRKLIISVDS 180
QY 181 RSVSLLPLEFRKDSYELQVRAGMPGSSYQGTWSESDPVI FQTQSEELKEGWNPHLLL 240
Db 181 RSVSLLPLEFRKDSYELQVRAGMPGSSYQGTWSESDPVI FQTQSEELKEGWNPHLLL 240
QY 241 LLLLVIVFIPAFWSLTKTHPLWRLWKIWA VSPERFPMPLYKGCSDGDFKRWGAPFTGSS 300
Db 241 LLLLVIVFIPAFWSLTKTHPLWRLWKIWA VSPERFPMPLYKGCSDGDFKRWGAPFTGSS 300
QY 301 LELGWPSPVSTLEVYSCHPSPRPAKRLQLTQLQEPALVESDGVKPSFWPTAQNSSG 360
Db 301 LELGWPSPVSTLEVYSCHPSPRPAKRLQLTQLQEPALVESDGVKPSFWPTAQNSSG 360
QY 361 SAYSEERDRPYGLVSIIDTVTLDAEGPCTWPCSCDDGYPALDLADGLESPGLEDPILLD 420
Db 361 SAYSEERDRPYGLVSIIDTVTLDAEGPCTWPCSCDDGYPALDLADGLESPGLEDPILLD 420
QY 421 AGTTVLSCGCVSAGSPGLGGLSLDLRLKPLADGEDWAGLPGWGRSPGCVSESEAGS 480
Db 421 AGTTVLSCGCVSAGSPGLGGLSLDLRLKPLADGEDWAGLPGWGRSPGCVSESEAGS 480
QY 481 PLAGLDMDTDSGFGVSDCSPEVCDFTSPGDEGPPRSYLRQWVVIPTLSSPGPQAS 538
Db 481 PLAGLDMDTDSGFGVSDCSPEVCDFTSPGDEGPPRSYLRQWVVIPTLSSPGPQAS 538

RESULT 12
US-10-620-169-4
; Sequence 4, Application US/10620169
; Publication No. US20040136954A1
; GENERAL INFORMATION:
; APPLICANT: Grusby, Michael J
; APPLICANT: Wurster, Andrea
; APPLICANT: Young, Deborah
; APPLICANT: Collins, Mary
; APPLICANT: Whitters, Matthew
; TITLE OF INVENTION: Methods and Compositions for Modulating T Helper (TH)
; TITLE OF INVENTION: Cell Development and Function
; FILE REFERENCE: 22058-585
; CURRENT APPLICATION NUMBER: US/10/620,169
; CURRENT FILING DATE: 2003-07-15
; PRIOR APPLICATION NUMBER: 60/396,160
; PRIOR FILING DATE: 2003-07-15
; PRIOR APPLICATION NUMBER: 60/403,001
; PRIOR FILING DATE: 2003-08-12
; NUMBER OF SEQ ID NOS: 13
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 4
; LENGTH: 538
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-620-169-4

Query Match 100.0%; Score 2958; DB 16; Length 538;
Best Local Similarity 100.0%; Pred. No. 2.3e-228;
Matches 538; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 MPRGWAAPLLLLLQGGGCPDLVCYTDYLTQVTCILEMNNLHPSTLTLTWQDQYEELKD 60
Db 1 MPRGWAAPLLLLLQGGGCPDLVCYTDYLTQVTCILEMNNLHPSTLTLTWQDQYEELKD 60
QY 61 EATCSLHRSAHNATHATYTCMDVHFHMADDIFSVNITDQSGNYSQCGSFLLAESIKP 120
Db 61 EATCSLHRSAHNATHATYTCMDVHFHMADDIFSVNITDQSGNYSQCGSFLLAESIKP 120
QY 121 APPFNVTTFSGQYNISWRSDYEDPAFYMLKGLQYELQYRNRPDPAVSPRRKLI SVDS 180
Db 121 APPFNVTTFSGQYNISWRSDYEDPAFYMLKGLQYELQYRNRPDPAVSPRRKLI SVDS 180
QY 181 RSVSLLPLEFRKDSYELQVRAGMPGSSYQGTWSESDPVI FQTQSEELKEGWNPHLLL 240
Db 181 RSVSLLPLEFRKDSYELQVRAGMPGSSYQGTWSESDPVI FQTQSEELKEGWNPHLLL 240
QY 241 LLLLVIPIPAFWSLKTPLRLWKIWA VSPERFPMPL YKGCSDGDFKKWVGAPFTGSS 300
Db 241 LLLLVIPIPAFWSLKTPLRLWKIWA VSPERFPMPL YKGCSDGDFKKWVGAPFTGSS 300
QY 301 LELGWSPEVSTLEVYSCHPSPRPAKRLQLTELQEPALVESDGVKPKSPFWPTAQN SGG 360
Db 301 LELGWSPEVSTLEVYSCHPSPRPAKRLQLTELQEPALVESDGVKPKSPFWPTAQN SGG 360
QY 361 SAYSEERDRPYGLVSDITVTVLDAEGPCTWPCSCDDGYPALDLADGLESPGLDPLLD 420
Db 361 SAYSEERDRPYGLVSDITVTVLDAEGPCTWPCSCDDGYPALDLADGLESPGLDPLLD 420
QY 421 AGTTVLSGCCVSAGSPGLGGPLGSLLDRLKPLADGEDWAGGLPWGGRSPGVSSSEAGS 480
Db 421 AGTTVLSGCCVSAGSPGLGGPLGSLLDRLKPLADGEDWAGGLPWGGRSPGVSSSEAGS 480
QY 481 PLAGLDMDTDFSGFVSGDCSSPVECDFTSPGDEGPPRSYLQWVVI PPLSSPGQAS 538
Db 481 PLAGLDMDTDFSGFVSGDCSSPVECDFTSPGDEGPPRSYLQWVVI PPLSSPGQAS 538

RESULT 13
US-10-715-998-2
; Sequence 2, Application US/10715998
; Publication No. US20040204562A1

; GENERAL INFORMATION:
; APPLICANT: Presnell, Scott R.
; APPLICANT: Conklin, Darrell C.
; APPLICANT: Novak, Julia E.
; APPLICANT: Hammond, Angela K.
; TITLE OF INVENTION: CYTOKINE RECEPTOR ZAPLHALL
; FILE REFERENCE: 98-55
; CURRENT APPLICATION NUMBER: US/10/715,998
; CURRENT FILING DATE: 2003-11-18
; PRIOR APPLICATION NUMBER: US/10/414,186
; PRIOR FILING DATE: 2003-04-14
; PRIOR APPLICATION NUMBER: US/09/404,641
; PRIOR FILING DATE: 1999-09-23
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: US 60/100,896
; PRIOR FILING DATE: EARLIER FILING DATE: 1998-09-23
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: US 60/123,546
; PRIOR FILING DATE: EARLIER FILING DATE: 1999-03-09
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: US 60/142,574
; PRIOR FILING DATE: EARLIER FILING DATE: 1999-07-06
; NUMBER OF SEQ ID NOS: 91
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 2
; LENGTH: 538
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-715-998-2

Query Match 100.0%; Score 2958; DB 16; Length 538;
Best Local Similarity 100.0%; Pred. No. 2.3e-228;
Matches 538; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 MPRGWAAPLLLLLQGGGCPDLVCYTDYLTQVTCILEMNNLHPSTLTLTWQDQYEELKD 60
Db 1 MPRGWAAPLLLLLQGGGCPDLVCYTDYLTQVTCILEMNNLHPSTLTLTWQDQYEELKD 60
QY 61 EATCSLHRSAHNATHATYTCMDVHFHMADDIFSVNITDQSGNYSQCGSFLLAESIKP 120
Db 61 EATCSLHRSAHNATHATYTCMDVHFHMADDIFSVNITDQSGNYSQCGSFLLAESIKP 120
QY 121 APPFNVTTFSGQYNISWRSDYEDPAFYMLKGLQYELQYRNRPDPAVSPRRKLI SVDS 180
Db 121 APPFNVTTFSGQYNISWRSDYEDPAFYMLKGLQYELQYRNRPDPAVSPRRKLI SVDS 180
QY 181 RSVSLLPLEFRKDSYELQVRAGMPGSSYQGTWSESDPVI FQTQSEELKEGWNPHLLL 240
Db 181 RSVSLLPLEFRKDSYELQVRAGMPGSSYQGTWSESDPVI FQTQSEELKEGWNPHLLL 240
QY 241 LLLLVIPIPAFWSLKTPLRLWKIWA VSPERFPMPL YKGCSDGDFKKWVGAPFTGSS 300
Db 241 LLLLVIPIPAFWSLKTPLRLWKIWA VSPERFPMPL YKGCSDGDFKKWVGAPFTGSS 300
QY 301 LELGWSPEVSTLEVYSCHPSPRPAKRLQLTELQEPALVESDGVKPKSPFWPTAQN SGG 360
Db 301 LELGWSPEVSTLEVYSCHPSPRPAKRLQLTELQEPALVESDGVKPKSPFWPTAQN SGG 360
QY 361 SAYSEERDRPYGLVSDITVTVLDAEGPCTWPCSCDDGYPALDLADGLESPGLDPLLD 420
Db 361 SAYSEERDRPYGLVSDITVTVLDAEGPCTWPCSCDDGYPALDLADGLESPGLDPLLD 420
QY 421 AGTTVLSGCCVSAGSPGLGGPLGSLLDRLKPLADGEDWAGGLPWGGRSPGVSSSEAGS 480
Db 421 AGTTVLSGCCVSAGSPGLGGPLGSLLDRLKPLADGEDWAGGLPWGGRSPGVSSSEAGS 480
QY 481 PLAGLDMDTDFSGFVSGDCSSPVECDFTSPGDEGPPRSYLQWVVI PPLSSPGQAS 538
Db 481 PLAGLDMDTDFSGFVSGDCSSPVECDFTSPGDEGPPRSYLQWVVI PPLSSPGQAS 538

RESULT 14
US-10-872-087-2
; Sequence 2, Application US/10872087
; Publication No. US20040235743A1
; GENERAL INFORMATION:

; APPLICANT: Sprecher, Cindy A.
; APPLICANT: Novak, Julia E.
; APPLICANT: West, James W.
; APPLICANT: Holly, Richard D.
; APPLICANT: Nelson, Andrew J.
; APPLICANT: Hammond, Stacey R.
; TITLE OF INVENTION: SOLUBLE ZALPHA11 CYTOKINE RECEPTORS
; FILE REFERENCE: 00-22D1

; CURRENT APPLICATION NUMBER: US/10/872,087

; CURRENT FILING DATE: 2004-06-18

; PRIOR APPLICATION NUMBER: US 60/194,731

; PRIOR FILING DATE: 2000-04-05

; PRIOR APPLICATION NUMBER: US 60/222,121

; PRIOR FILING DATE: 2000-07-28

; PRIOR APPLICATION NUMBER: US 09/825,561

; PRIOR FILING DATE: 2001-04-03

; NUMBER OF SEQ ID NOS: 86

; SOFTWARE: FastSeq for Windows Version 3.0

; SEQ ID NO 2

; LENGTH: 538

; TYPE: PRT

; ORGANISM: Homo sapiens

US-10-872-087-2

Query Match 100.0%; Score 2958; DB 16; Length 538;

Best Local Similarity 100.0%; Pred. No. 2.3e-228;

Matches 538; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy 1 MPRGAAAPLLLLLQGGGCPDLVCYTDYLTQVTCILEMNLHPSTLTLTWQDQYEELKD 60
Db 1 MPRGAAAPLLLLLQGGGCPDLVCYTDYLTQVTCILEMNLHPSTLTLTWQDQYEELKD 60

Qy 61 EATCSLHSAHNATHATYTCMDVDFHFMADDIFSVNITDQSGNYSQCGSFLLAESIKP 120
Db 61 EATCSLHSAHNATHATYTCMDVDFHFMADDIFSVNITDQSGNYSQCGSFLLAESIKP 120

Qy 121 APPFNVTTFSGQYNISWRSDYEDPAFYMLKGKLYQLQYLRNRGDPWAVSPRRKLISVDS 180
Db 121 APPFNVTTFSGQYNISWRSDYEDPAFYMLKGKLYQLQYLRNRGDPWAVSPRRKLISVDS 180

Qy 181 RSVLLPLEFRKDSSEYELQVRAGMPGSSYQGTWSEWSDPVIQTQSEELKEGWNPHLL 240
Db 181 RSVLLPLEFRKDSSEYELQVRAGMPGSSYQGTWSEWSDPVIQTQSEELKEGWNPHLL 240

Qy 241 LLLLVIVIFAPWSLKTPLWRLWKKIWAVSPERFPMPLKYGCGDFKWWGAPFTGSS 300
Db 241 LLLLVIVIFAPWSLKTPLWRLWKKIWAVSPERFPMPLKYGCGDFKWWGAPFTGSS 300

Qy 301 LELGWSPEVPSTLEVYCHPPRSPAKRLQLTELQEPALVESDGVKPSFWPTAQNSGG 360
Db 301 LELGWSPEVPSTLEVYCHPPRSPAKRLQLTELQEPALVESDGVKPSFWPTAQNSGG 360

Qy 361 SAYSEERDRPYGLVSIIDTVTLDAEGPCTWPCSCDDGYPALDLDAGLESPGLEDPILLD 420
Db 361 SAYSEERDRPYGLVSIIDTVTLDAEGPCTWPCSCDDGYPALDLDAGLESPGLEDPILLD 420

Qy 421 AGTTVLSCGCVSAGSPGLGGPLGSLDLRLKPLADGEDWAGGLPWGGRSPCGVSESEAGS 480
Db 421 AGTTVLSCGCVSAGSPGLGGPLGSLDLRLKPLADGEDWAGGLPWGGRSPCGVSESEAGS 480

Qy 481 PLAGLDMDTFDSGFGVSDCSSPVECDFTSPGDEGPPRSYLQWVVIPTPLSSPGPQAS 538
Db 481 PLAGLDMDTFDSGFGVSDCSSPVECDFTSPGDEGPPRSYLQWVVIPTPLSSPGPQAS 538
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RESULT 15

US-10-787-442-115

; Sequence 115, Application US/10787442

; Publication No. US2004026065A1

; GENERAL INFORMATION:

; APPLICANT: Novak, Julia E.

; APPLICANT: Presnell, Scott R.

; APPLICANT: Sprecher, Cindy A.

; APPLICANT: Foster, Donald C.

; APPLICANT: Holly, Richard D.
; APPLICANT: Gross, Jane A.
; APPLICANT: Johnston, Janet V.
; APPLICANT: Nelson, Andrew J.
; APPLICANT: Dillon, Stacey R.
; APPLICANT: Hammond, Angela K.
; TITLE OF INVENTION: NOVEL CYTOKINE ZALPHA11 LIGAND
; FILE REFERENCE: 99-16

; CURRENT APPLICATION NUMBER: US/10/787,442

; CURRENT FILING DATE: 2004-02-26

; PRIOR APPLICATION NUMBER: US/09/522,217

; PRIOR FILING DATE: 2000-03-09

; PRIOR APPLICATION NUMBER: US 60/123,547

; PRIOR FILING DATE: 1999-03-09

; PRIOR APPLICATION NUMBER: US 60/123,904

; PRIOR FILING DATE: 1999-03-11

; PRIOR APPLICATION NUMBER: US 60/142,013

; PRIOR FILING DATE: 1999-07-01

; NUMBER OF SEQ ID NOS: 115

; SOFTWARE: FastSeq for Windows Version 3.0

; SEQ ID NO 115

; LENGTH: 538

; TYPE: PRT

; ORGANISM: Homo sapiens

US-10-787-442-115

Query Match 100.0%; Score 2958; DB 16; Length 538;

Best Local Similarity 100.0%; Pred. No. 2.3e-228;

Matches 538; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy 1 MPRGAAAPLLLLLQGGGCPDLVCYTDYLTQVTCILEMNLHPSTLTLTWQDQYEELKD 60
Db 1 MPRGAAAPLLLLLQGGGCPDLVCYTDYLTQVTCILEMNLHPSTLTLTWQDQYEELKD 60

Qy 61 EATCSLHSAHNATHATYTCMDVDFHFMADDIFSVNITDQSGNYSQCGSFLLAESIKP 120
Db 61 EATCSLHSAHNATHATYTCMDVDFHFMADDIFSVNITDQSGNYSQCGSFLLAESIKP 120

Qy 121 APPFNVTTFSGQYNISWRSDYEDPAFYMLKGKLYQLQYLRNRGDPWAVSPRRKLISVDS 180
Db 121 APPFNVTTFSGQYNISWRSDYEDPAFYMLKGKLYQLQYLRNRGDPWAVSPRRKLISVDS 180

Qy 181 RSVLLPLEFRKDSSEYELQVRAGMPGSSYQGTWSEWSDPVIQTQSEELKEGWNPHLL 240
Db 181 RSVLLPLEFRKDSSEYELQVRAGMPGSSYQGTWSEWSDPVIQTQSEELKEGWNPHLL 240

Qy 241 LLLLVIVIFAPWSLKTPLWRLWKKIWAVSPERFPMPLKYGCGDFKWWGAPFTGSS 300
Db 241 LLLLVIVIFAPWSLKTPLWRLWKKIWAVSPERFPMPLKYGCGDFKWWGAPFTGSS 300

Qy 301 LELGWSPEVPSTLEVYCHPPRSPAKRLQLTELQEPALVESDGVKPSFWPTAQNSGG 360
Db 301 LELGWSPEVPSTLEVYCHPPRSPAKRLQLTELQEPALVESDGVKPSFWPTAQNSGG 360

Qy 361 SAYSEERDRPYGLVSIIDTVTLDAEGPCTWPCSCDDGYPALDLDAGLESPGLEDPILLD 420
Db 361 SAYSEERDRPYGLVSIIDTVTLDAEGPCTWPCSCDDGYPALDLDAGLESPGLEDPILLD 420

Qy 421 AGTTVLSCGCVSAGSPGLGGPLGSLDLRLKPLADGEDWAGGLPWGGRSPCGVSESEAGS 480
Db 421 AGTTVLSCGCVSAGSPGLGGPLGSLDLRLKPLADGEDWAGGLPWGGRSPCGVSESEAGS 480

Qy 481 PLAGLDMDTFDSGFGVSDCSSPVECDFTSPGDEGPPRSYLQWVVIPTPLSSPGPQAS 538
Db 481 PLAGLDMDTFDSGFGVSDCSSPVECDFTSPGDEGPPRSYLQWVVIPTPLSSPGPQAS 538
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Search completed: July 9, 2005, 12:00:42

Job time : 165 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: July 9, 2005, 11:29:09 ; Search time 178 Seconds
(without alignments)
1547.745 Million cell updates/sec

Title: US-10-620-169-4

Perfect score: 2958

Sequence: 1 MPRGWAPLILLILQLGGWGC.....YLQWVWVPPSLSPGPGQAS 538

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1612378 seqs, 512079187 residues

Total number of hits satisfying chosen parameters: 1612378

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : UniProt_03.*

1: uniprot_sprot.*

2: uniprot_trembl.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	2958	100.0	538	1 I21R_HUMAN	Q9hbe5 homo sapien
2	1735.5	58.7	529	1 I21R_MOUSE	Q9jhx3 mus musculus
3	872	29.5	268	2 Q6PE08	Q6peu8 mus musculus
4	286	9.7	512	2 Q6UAP3	Q6uap3 tetraodon n
5	278	9.4	551	1 IL2B_HUMAN	P14784 homo sapien
6	250	8.5	890	2 Q9ZL10	Q9z1a0 cavia porce
7	248	8.4	537	1 IL2B_RAT	P26896 rattus norv
8	247.5	8.4	539	1 IL2B_MOUSE	P16297 mus musculus
9	245.5	8.3	539	2 Q8R308	Q8r308 mus musculus
10	243.5	8.2	539	2 Q8CBU1	Q8cbu1 mus musculus
11	233	7.9	896	1 CYRB_MOUSE	P26955 mus musculus
12	231	7.8	896	2 Q8QZ19	Q8qzx9 mus musculus
13	226	7.6	529	2 Q8UAP7	Q8uap7 tetraodon n
14	221.5	7.5	468	1 IL9R_MOUSE	Q01114 mus musculus
15	221.5	7.5	631	2 Q6UAN4	Q6uan4 tetraodon n
16	218.5	7.4	419	2 Q6UAN6	Q6uan6 tetraodon n
17	218.5	7.4	878	1 IL3B_MOUSE	P26954 mus musculus
18	215	7.3	522	1 IL9R_HUMAN	Q01113 homo sapien
19	213.5	7.2	467	2 Q83216	Q83216 rattus norv
20	213	7.2	508	1 EPOR_HUMAN	P19235 homo sapien
21	211.5	7.2	896	2 Q64146	Q64146 rattus sp.
22	211.5	7.2	896	2 Q78ZFS	Q78zfs rattus norv
23	210	7.1	469	2 Q8C2G1	Q8c2g1 mus musculus
24	206	7.0	889	2 Q6NSJ8	Q6nsj8 homo sapien
25	206	7.0	897	1 CYRB_HUMAN	P29272 homo sapien
26	204.5	6.9	903	2 Q6ICE0	Q6ice0 homo sapien
27	201	6.8	507	1 EPOR_MOUSE	P14753 mus musculus
28	199	6.7	509	1 EPOR_PIG	Q9myz9 sus scrofa
29	198	6.7	441	2 Q6UAP5	Q6uap5 tetraodon n
30	195	6.6	507	1 EPOR_RAT	Q07303 rattus norv
31	193.5	6.5	825	1 IL4R_HUMAN	P24394 homo sapien

32	193	6.5	198	2 Q6UA82	Q6ua82 canis famil
33	192	6.5	830	1 IL4R_PIG	Q86325 sus scrofa
34	189.5	6.4	810	1 IL4R_MOUSE	P16382 mus musculus
35	183	6.2	884	2 Q6UAM6	Q6uam6 tetraodon n
36	176	5.9	371	1 CRL2_HUMAN	Q9hc73 homo sapien
37	171	5.8	348	2 Q8AUF2	Q8aup2 gallus gall
38	170.5	5.8	801	1 IL4R_RAT	Q63257 rattus norv
39	170	5.7	809	1 IL4R_HORSE	Q6wg24 equus cabal
40	168.5	5.7	635	1 TPOR_HUMAN	P40238 homo sapien
41	168	5.7	369	1 CYRG_MOUSE	P34902 mus musculus
42	164.5	5.6	418	2 Q95N14	Q95n14 ovine aries
43	161	5.4	831	1 PRLR_MELGA	Q91094 melagris g
44	160	5.4	387	2 Q95N13	Q95n13 ovine aries
45	159	5.4	831	1 PRLR_CHICK	Q04594 gallus gall

ALIGNMENTS

RESULT 1
121R_HUMAN
ID I21R_HUMAN STANDARD; PRT; 538 AA.
AC Q9HBE5; Q96HZ1; Q9HB91;
DT 28-FEB-2003 (Rel. 41, Created)
DT 28-FEB-2003 (Rel. 41, Last sequence update)
DT 25-JAN-2005 (Rel. 46, Last annotation update)
DE Interleukin 21 receptor precursor (IL-21R) (Novel interleukin receptor) (UNQ3121/PRO10273).
GN Name=IL21R; Synonyms=NILR;
OS Homo sapiens (Human)
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=20531754; PubMed=11081504; DOI=10.1038/35040504;
RA Parrish-Novak J., Dillon S.R., Nelson A., Hammond A., Sprecher C., Gross J.A., Johnston J., Madden K., Xu W., West J., Schrader S., Burkhead S., Heipel M., Brandt C., Kujper J.L., Kramer J., Conklin D., Presnell S.R., Berry J., Shiota F., Bort S., Hamby K., Mudri S., Clegg C., Moore M., Grant F.J., Lofton-Day C., Gilbert T., Raymond F., Ching A., Yao L., Smith D., Webster P., Whitmore T., Maurer M., Kaushansky K., Holly R.D., Foster D.;
RT "Interleukin 21 and its receptor are involved in NK cell expansion and regulation of lymphocyte function."
RL Nature 408:57-63 (2000).
RN [2]
RP SEQUENCE FROM N.A.
RX MEDLINE=20481926; PubMed=11016959; DOI=10.1073/pnas.200360997;
RA Ozaki K., Kikly K., Michalovich D., Young P.R., Leonard W.J.;
RT "Cloning of a type I cytokine receptor most related to the IL-2 receptor beta chain."
RL Proc. Natl. Acad. Sci. U.S.A. 97:11439-11444 (2000).
RN [3]
RP SEQUENCE FROM N.A.
RX MEDLINE=22887296; PubMed=12975309; DOI=10.1101/gr.1293003;
RA Clark H.F., Gurney A.L., Abaya E., Baker K., Baldwin D., Brush J., Chen J., Chow B., Chui C., Crowley C., Currell B., Deuel B., Dowd P., Eaton D., Foster J., Grimaldi C., Gu Q., Hass P.E., Heldens S., Huang A., Kim H.S., Klimowski L., Jin Y., Johnson S., Lee J., Lewis L., Liao D., Mark M., Robbie E., Sanchez C., Schoenfeld J., Seshagiri S., Sattarab C., Singh J., Smith V., Stinson J., Vagts A., Vandlen R., Watanabe C., Wiedand D., Woods K., Xie M.-H., Yansura D., Yi S., Yu G., Yuan J., Zhang M., Zhang Z., Goddard A., Wood W.I., Godowski P., Gray A.;
RT "The secreted protein discovery initiative (SPDI), a large-scale effort to identify novel human secreted and transmembrane proteins: a bioinformatics assessment."
RL Genome Res. 13:2265-2270 (2003).
RN [4]
RP SEQUENCE FROM N.A. AND VARIANTS CYS-191; ARG-318 AND SER-484.
RA Rieder M.J., Arnel T.Z., Carrington D.P., Chung M.-W., Lee K.L., Poel C.L., Toth E.J., Yi Q., Nickerson D.A.;

05-JUL-2004 (Rel. 44, Last annotation update)
 Interleukin 21 receptor precursor (IL-21R) (Novel interleukin receptor) (lymphocyte receptor beta) (IL-beta) (Novel cytokine receptor NR8).
 Name=IL21r; Synonyms=NILr;
 Mus musculus (Mouse).
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 NCBI_TaxID=10090;
 [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=C57BL/6;
 RX MEDLINE=20531754; PubMed=11081504; DOI=10.1038/35040504;
 RA Parrish-Novak J., Dillon S.R., Nelson A., Hammond A., Sprecher C., Gross J.A., Johnston J., Madden K., Xu W., West J., Schrader S., Burkhead S., Heipel M., Brandt C., Kuipjer J.L., Kramer J., Conklin D., Presnell S.R., Berry J., Shioti F., Bort S., Hamby K., Mudri S., Clegg C., Moore M., Grant F.J., Lofton-Day C., Gilbert T., Raymond P., Ching A., Yao L., Smith D., Webster P., Whitmore T., Maurer M., Kaushansky K., Holly R.D., Foster D.;
 "Interleukin 21 and its receptor are involved in NK cell expansion and regulation of lymphocyte function.";
 Nature 408:57-63(2000).
 [2]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Spleen, and Thymus;
 RX MEDLINE=20481926; PubMed=11016959; DOI=10.1073/pnas.200360997;
 RA Ozaki K., Kikly K., Michalovich D., Young P.R., Leonard W.J.;
 "Cloning of a type I cytokine receptor most related to the IL-2 receptor beta chain.";
 Proc. Natl. Acad. Sci. U.S.A. 97:11439-11444(2000).
 [3]
 RP SEQUENCE FROM N.A.
 RA Donaldson D.D., Whitters M.J., Fitz L., Unger M., Finnerty H., Dagigian C., Lowe L., Wood C.R., Young D.A., Collins M.;
 "Chromosome 16p12 encodes a biologically active IL-2Rb related receptor with lymphoid restricted expression.";
 Submitted (JUN-2000) to the EMBL/GenBank/DBJ databases.
 [4]
 RP SEQUENCE FROM N.A.
 RC STRAIN=BALB/c;
 RA Nomura H., Yaguchi N., Maeda M., Hasegawa M.;
 "A novel cytokine receptor NR8 is closely mapped to IL-4R: polymorphism in Balb/c mouse.";
 Submitted (SEP-2000) to the EMBL/GenBank/DBJ databases.
 [5]
 RP SEQUENCE FROM N.A.
 RC STRAIN=A/J, B10.S/DvTe, C57BL/6J, NOD/LtJ, and SJL/J; TISSUE=Spleen;
 RA Gao J., Teuscher C.;
 "Mus musculus interleukin 21 receptor gene Il21r mRNA.";
 Submitted (JAN-2002) to the EMBL/GenBank/DBJ databases.
 RL FUNCTION: This is a receptor for interleukin-21.
 CC SUBUNIT: Heterodimer with the common gamma chain. Associates with JAK1.
 CC SUBCELLULAR LOCATION: Type I membrane protein.
 CC TISSUE SPECIFICITY: Selectively expressed in lymphoid tissues.
 CC Most highly expressed in thymus and spleen.
 CC DOMAIN: The WSXWS motif appears to be necessary for proper protein folding and thereby efficient intracellular transport and cell-surface receptor binding.
 CC DOMAIN: The box 1 motif is required for JAK interaction and/or activation.
 CC SIMILARITY: Belongs to the type I cytokine family of receptors.
 CC Subfamily 4.
 CC SIMILARITY: Contains 1 fibronectin type III domain.
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CC EMBL; AF254068; AAG29347.1; -
 DR EMBL; AF269134; AAG23420.1; -
 DR EMBL; AF279436; AAF86350.1; -
 DR EMBL; AB049137; BAB13736.1; -
 DR EMBL; AF477982; AAL82632.1; -
 DR EMBL; AF477983; AAL82633.1; -
 DR EMBL; AF477984; AAL82634.1; -
 DR EMBL; AF477985; AAL82635.1; -
 DR EMBL; AF477986; AAL82636.1; -
 DR MGI:1890475; IL21r.
 DR GO: 0004907; F:interleukin receptor activity; IDA.
 DR InterPro; IPR008957; FN_III-like.
 DR InterPro; IPR003331; Hemtreceptor_F1.
 DR PROSITE; PS01355; HEMATOPO RECS.F1; FALSE NEG.
 KW Glycoprotein; Polymorphism; Receptor; Signal; Transmembrane.
 FT SIGNAL 1 19
 FT CHAIN 20 529
 FT DOMAIN 20 237
 FT TRANSMEM 238 258
 FT DOMAIN 120 209
 FT SITE 214 218
 FT SITE 266 274
 FT DISULFID 25 35
 FT DISULFID 65 81
 FT CARBOHYD 73 73
 FT CARBOHYD 97 97
 FT CARBOHYD 104 104
 FT CARBOHYD 125 125
 FT CARBOHYD 182 182
 FT VARIANT 69 69
 FT VARIANT 200 200
 FT VARIANT V -> M (in strain BALB/c and strain SJL/J).
 FT VARIANT J).
 SQ SEQUENCE 529 AA; 58354 MW; 8B41816B0D426581 CRC64;
 Query Match 58.7%; Score 1735.5; DB 1; Length 529;
 Best Local Similarity 62.7%; Pred. No. 1.1e-109;
 Matches 340; Conservative 49; Mismatches 136; Indels 17; Gaps 6;
 QY 1 MPRGWAAPLALLLGGGCPDLVCTDYDTVLTVCILEMNLHPSTLTLTWQDQVEELKD 60
 DB 1 MERGPVAALLLLHGAWSCLDLTCYDTLTWTTTCITRSPNPSILSTWQDEYELQD 60
 QY 61 EATCSLHRSAHNATHATYTCMDVHFPMADDIFSVNITDQSGNYSCQSGFLAESIKP 120
 DB 61 QETCSLHRSAGNTHIWTTCMRLSQFLSDEVFIVNVTDSGNNSCGSGFVLAESIKP 120
 QY 121 APPFNVTTFSGQYNISWRSDYEDPAFYLKGLQYLRNRGDPMAVSPRRKLIISVDS 180
 DB 121 APPLNVTVAESGRYDISWDSAYDEPSNVYLRGLQYLRNLRDPYAVRPVTKLIISVDS 180
 QY 181 RSVSLLPLEFRKDSYELQVAGPMGSSYOGTWSNSDPVTFQTSSELKEGNPHLL 240
 DB 181 RNVSLLPEEFKDSYQLQVRAAPQPGTSFGTSWNSDPVTFQTSAGEAGDPHMLL 240
 QY 241 LLLVIVIPAFWSLKTPLRLWKIWA-VPSPERFFMPLYKGCSDGFKKVVAGPPTGS 299
 DB 241 LLAVLIIVL-VFMGLKHLPLRLWKIWA-VPTPESFPQLYRHSNGFKKVVNTPTAS 299
 QY 300 SLELGPSPVPTSTLEVYSCHPSPAKRQLQTELQEPALVESDGVPKPSFW---PTAQ 356
 DB 300 SIELVPSQSTTTTSL-----HLSLYPAKEKKFPGLGLEEQLECDGMSEPGHWCIPLAA 354
 QY 357 NSGSAYSEEDRDRPGLVSDITVTVLDAEGCTWPCSCDDGYPALDLDAGLSPGL 416
 DB 355 QGAVSAYSEEDRDRPGLVSDITVTVDAGELCVMPSCDDGYPAAMNLDAGRESGPN 414
 QY 417 PLLDAGTTVLSCGVSAGSGPLGSLDLRLKPLADGSDWAGGLPWGGRSPGVSES 476
 DB 415 LLLVTDPAFLSCGVSGLRGLGSGPSLLDLRLSLPAKEGDWADPTWRTGSPGVSES 474

Qy	477	EGASPLAGLMDMTFDSGFGVSGDCSPVCDFTSFCDGPRSYLRQWVVPPLSLSGPQ	537
Db	475	EGASPG-PLGLMDMTFDSGFGAGSCGSPVET-----DGPPRSYLRLQWVVRTPPVDGSAQ	537
Qy	537	AS 538	
Db	528	SS 529	
RESULT 3			
Q6PEU8			
ID	Q6PEU8	PRELIMINARY; PRT; 268 AA.	
AC	Q6PEU8;		
DT	05-JUL-2004 (TrEMBLrel. 27, Created)		
DT	05-JUL-2004 (TrEMBLrel. 27, Last sequence update)		
DT	05-JUL-2004 (TrEMBLrel. 27, Last annotation update)		
DE	IL21r protein		
OS	Mus musculus (Mouse).		
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;		
OC	Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.		
OX	NCBI_TaxID=10090;		
RN	[1]		
SEQUENCE FROM N.A.			
RP	STRAIN=129; TISSUE=Mammary tumor. Brcal-/fl;		
RC	MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;		
RA	Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,		
RA	Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,		
RA	Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,		
RA	Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Haieh F.,		
RA	Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,		
RA	Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,		
RA	Brownstein M.J., Usdin T.B., Toshikiyuki S., Carninci P., Prange C.,		
RA	Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,		
RA	Boesak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,		
RA	Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,		
RA	Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,		
RA	Fahey J., Helton E., Kettman M., Madan A., Rodrigues S., Sanchez A.,		
RA	Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,		
RA	Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,		
RA	Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,		
RA	Krzywinski M.I., Skalska U., Smallus D.E., Schnerch A., Schein J.E.,		
RA	Jones S.J., Marra M.A.;		
RT	"Generation and initial analysis of more than 15,000 full-length human		
RT	and mouse cDNA sequences."		
RL	Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).		
RN	[2]		
SEQUENCE FROM N.A.			
RP	STRAIN=129; TISSUE=Mammary tumor. Brcal-/fl;		
RC	Strausberg R.;		
RA	Submitted (SEP-2003) to the EMBL/GenBank/DBJ databases.		
RL	EMBL; BC057861; AAH57861.1; -		
DR	GO; GO:0005615; C:extracellular space; TAS.		
DR	GO; GO:0004907; F:interleukin receptor activity; IDA.		
DR	InterPro; IPR008957; FN.III-like.		
SQL	SEQUENCE 268 AA; 30116 MW; B2EBE0C31ACD6DA8 CRC64;		
Query Match 29.5%; Score 872; DB 2; Length 268;			
Best Local Similarity 69.6%; Pred. No. 2.3e-59;			
Matches 158; Conservative 30; Mismatches 39; Indels 0; Gaps 0			
Qy	1	MPRGWAAPLLLLLLLOGGGCPDLVCYTDYLTQVICILEMNLHPSTLTLTWQDQYBELKD	60
Db	1	MPRGVPVALLLLILHGANSCLDLCYTDYLTWITTCVLETRSPNPISLSLTWQDEYELQD	60
Qy	61	EATSCSLRSAHNATHATYTCMDVFFHMADDIFSNTIDSGNYSQCSFLLASIKP	120
Db	61	QETFCSLRSGHNTTHIWTCHMRLSQFLSDDEVFVNVNTDQSGNNSQCSGFVLAISIKP	120
Qy	121	APPFNVTVTFSGQYNISWSDYEDPAFYMLGKQLQYELQYVNRCDPMVSPRKLISVDS	180
Db	121	APPLNVTVAFSGRYDSDWSADYEDSNFYMLGKQLQYELQYVNRKLRDPAVVRPVTKLISVDS	180
Qy	181	RSVSLPLPLEFRKDSGSVELQVRAGMPGSSYOGTWTSEWSDPVIFOTOS 227	

[illegible]

QY 327 KRLQLTELQPAELVSDGVKPSFWFTQNSGGSAYSEERDRPYGLVSDITVTVDAB- 385
 DB 329 PKLQAO--AHPLLGSDWG-----SQSRGLA-----GPISHTVTLSEEE 368
 QY 386 -----GPTWPCSCEDDGYPALDLDAGLSPGLDPLLDAGTTVLSCGCVSAGSP 436
 DB 369 FEEGTSQSACVLRSDQRESEFVFDWKEQAANGLEE-----AASGLP 414
 QY 437 GLGGPIGLSLDRKPLPADGEDWAGLPGGRSPGGVS-----ESRAGSPLAGLMD 488
 DB 415 -----PVLQQRASRSSGEGDDVPLPHQFFRAERVSLDLSLALNDQSDGYP--HVDLD 465
 QY 489 TPDGFGVSDCSPVECDTSPGEGPP-----RSLQWVV 525
 DB 466 TIDSGF--GEYNSP-----GASPGADQTSLSHEHNLHNSYVQMWV 505

RESULT 5
 IL2B HUMAN STANDARD; PRT; 551 AA.
 AC P14784;
 DT 01-APR-1990 (Rel. 14, Created)
 DT 01-APR-1990 (Rel. 14, Last sequence update)
 DT 25-OCT-2004 (Rel. 45, Last annotation update)
 DE Interleukin-2 receptor beta chain precursor (IL-2 receptor) (P70-75)
 DE (High affinity IL-2 receptor beta subunit) (CD122 antigen).
 GN Names-IL2RB;
 OS Homo sapiens (Human).
 OC Eukaryota; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 OC NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=89242117; PubMed=2785715;
 RA Hatakeyama M., Tsudo M., Minamoto S., Kono T., Doi T., Miyata T.,
 R# Miyasaka M., Taniguchi T.;
 RT "Interleukin-2 receptor beta chain gene: generation of three receptor
 RT forms by cloned human alpha and beta chain cDNA's";
 RL Science 244:551-556(1989).
 RN [2]
 RP SEQUENCE FROM N.A.
 RA Rieder M.J., Amel T.Z., Carrington D.P., Ozuna M., Kuldanek S.A.,
 RA Rajkumar N., Toth E.J., Yi Q., Nickerson D.A.;
 RT "SeattlesNP. NHLBI HL6682 program for genomic applications, UW-
 RT FHCR, Seattle, WA (URL: <http://pga.gs.washington.edu>).";
 RL Submitted (JUN-2002) to the EMBL/GenBank/DBJ databases.
 RN [3]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=20057165; PubMed=10591208; DOI=10.1038/990031;
 RA Dunham I., Hunt A.R., Collins J.E., Bruskewich R., Beare D.M.,
 RA Clamp M., Smink L.J., Ainscough R., Almeida J.P., Babbage A.K.,
 RA Baguley C., Bailey J., Barlow K.F., Bates K.N., Beasley O.P.,
 RA Bird C.P., Blakey S.E., Bridgeman A.M., Buck D., Burgess J.,
 RA Burrill W.D., Burton J., Carter C., Carter N.P., Chen Y., Clark G.,
 RA Clegg S.M., Cobley V.E., Cole C.G., Collier R.E., Connor R.,
 RA Conroy D., Corby N.R., Coville G.J., Cox A.V., Davis J., Dawson E.,
 RA Dhami P.D., Dockree C., Dodsworth S.J., Durbin R.M., Ellington A.G.,
 RA Evans K.L., Fey J.M., Fleming K., French L., Garner A.A.,
 RA Gilbert J.G.R., Goward M.E., Grafham D.V., Griffiths M.N.D., Hall C.,
 RA Hall R.E., Hall-Tamlyn G., Heathcote R.W., Ho S., Holmes S.,
 RA Hunt S.E., Jones M.C., Kershaw J., Kimberley A.M., King A.,
 RA Laird G.K., Langford C.F., Leversha M.A., Lloyd C., Lloyd D.M.,
 RA Martyn I.D., Mashreghi-Mohammadi M., Matthews L.H., Mccann O.T.,
 RA McLaren S., McMurray A.A., Milne S.A., Mortimore B.J.,
 RA Odell C.N., Pavitt R., Pearce A.V., Pearson D., Phillimore B.J.C.T.,
 RA Phillips S.H., Plumb R.W., Ramsay H., Ramsey Y., Rogers L., Ross M.T.,
 RA Scott C.E., Sehra H.K., Skuce C.D., Smalley S., Smith M.L.,
 RA Soderlund C., Spragon L., Steward C.A., Sulston J.E., Swann R.M.,
 RA Vaudin M., Wall M., Wallis J.M., Whiteley M.N., Willey D.L.,
 RA Williams L., Williams S.A., Williamson H., Wilmer T.E., Wilming L.,
 RA Wright C.L., Hubbard T., Bentley D.R., Beck S., Rogers J., Shimizu N.,
 RA Minoshima S., Kawasaki K., Sasaki T., Asakawa S., Kudoh J.,

Shintani A., Shibuya K., Yoshizaki Y., Aoki N., Mitsuyama S.,
 Roe B.A., Chen F., Chu L., Crabtree J., Deschamps S., Do A., Do T.,
 Dorman A., Fang F., Fu Y., Hua A., Kanton S., Lai H., Lao H.I.,
 Lewis J., Lewis S., Lin S.-P., Loh P., Malaj E., Nguyen T., Pan H.,
 Phan S., Qi S., Qian Y., Ray L., Ren Q., Shaull S., Sloan D., Song L.,
 Wang Q., Wang Y., Wang Z., White J., Willingham D., Wu H., Yao Z.,
 Zhan M., Zhang G., Chisoe S., Murray J., Miller N., Minx P.,
 Fulcon R., Johnson D., Bemis G., Bentley D., Bradshaw H., Bourne S.,
 Cordes M., Du Z., Fulton L., Goela D., Graves T., Hawkins J.,
 Hinds K., Kemp K., Latreille P., Layman D., Ozersky P., Rohlfing T.,
 Rofe P., Walker C., Wamsley A., Wohlmann P., Pepin K., Nelson J.,
 Korfi I., Bedell J.A., Hillier L.W., Mardis E., Waterston R.,
 Wilson R., Emanuel B.S., Shaikh T., Kurahashi H., Saita S.,
 Budarf M.L., McDermid H.E., Johnson A., Wong A.C.C., Morrow B.E.,
 Edelmann L., Kim U.J., Shizuya H., Simon M.I., Dumanski J.P.,
 Peyraud M., Kedra D., Seroussi E., Fransson I., Tapia I., Bruder C.E.,
 O'Brien K.P., Wilkison P., Bodenteich A., Hartman K., Hu X.,
 Khan A.S., Lane L., Tilahun Y., Wright H.;
 RT "The DNA sequence of human chromosome 22.";
 RL Nature 402:489-495(1999).
 RN [4]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Lung;
 RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
 RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G., Schuler G.D.,
 RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
 RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
 RA Hopkins R.P., Jordan H., Moore T., Max S.I., Wang J., Hsieh P.,
 RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
 RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
 RA Brownstein M.J., Ustin T.B., Toshiyuki S., Carninci P., Prange C.,
 RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullany S.J.,
 RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
 RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
 RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
 RA Fahy J., Helton E., Kettner M., Madan A., Rodriguez S., Sanchez A.,
 RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
 RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
 RA Rodriguez A.C., Grinstead J., Schmutz J., Myers R.M.,
 RA Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smalish D.E.,
 RA Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;
 RT "Generation and initial analysis of more than 15,000 full-length human
 RT and mouse cDNA sequences.";
 RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
 RN [5]
 RP 3D-STRUCTURE MODELING OF 31-230.
 RX MEDLINE=95111955; PubMed=7529123;
 RA Bamorough P., Hedgescock C.J., Richards W.G.;
 RT "The interleukin-2 and interleukin-4 receptors studied by molecular
 RT modelling.";
 RL Structure 2:839-851(1994).
 CC -!- FUNCTION: Receptor for interleukin 2. This beta subunit is
 CC involved in receptor mediated endocytosis and transduces the
 CC mitogenic signals of IL2.
 CC -!- SUBUNIT: Noncovalent dimer of an alpha and a beta chains. IL2R
 CC exists in 3 different forms: a high affinity dimer, an
 CC intermediate affinity monomer (beta chain), and a low affinity
 CC monomer (alpha chain). The high and intermediate affinity forms
 CC also associate with a gamma chain.
 CC -!- SUBCELLULAR LOCATION: Type I membrane protein.
 CC -!- DOMAIN: The WSXWS motif appears to be necessary for proper protein
 CC folding and thereby efficient intracellular transport and cell-
 CC surface receptor binding.
 CC -!- DOMAIN: The box 1 motif is required for JAK interaction and/or
 CC activation.
 CC -!- SIMILARITY: Belongs to the type I cytokine family of receptors.
 CC Subfamily 4.
 CC -!- SIMILARITY: Contains 1 fibronectin type III domain.
 CC -!- DATABASE: NAME=PROW; NOTE=CD guide CD122 entry;
 CC WWW="http://www.ncbi.nlm.nih.gov/prov/cd/cd122.htm".
 CC -----
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 CC between the Swiss Institute of Bioinformatics and the EMBL outstation -

the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See <http://www.isb-sib.ch/announce/> or send an email to license@isb-sib.ch).

DR EMBL; M26062; AAA59143.1; --
 DR EMBL; AF517934; AAM54040.1; --
 DR EMBL; AL022314; -- NOT_ANNOTATED_CDS.
 DR EMBL; BC025691; AAH25691.1; --
 DR FIR; A30342; A30342.
 DR PDB; 1ILM; Model; B=31-230.
 DR PDB; 1ILN; Model; B=31-230.
 DR Genew; HGNC:6009; IL2RB.
 DR H-invDB; HIX0016437; --
 DR MW; 146710; --
 DR GO; GO:0005887; C:integral to plasma membrane; TAS.
 DR GO; GO:0004911; F:interleukin-2 receptor activity; TAS.
 DR GO; GO:0006461; P:protein complex assembly; TAS.
 DR GO; GO:0007165; P:signal transduction; TAS.
 DR InterPro; IPR002996; Cytnk_recept_B/G.
 DR InterPro; IPR008957; FN_III-like.
 DR InterPro; IPR003531; HemtreceptS_F1.
 DR PROSITE; PS0853; FN3; 1.
 DR PROSITE; PS01355; HEMATOPO_REC_S_F1; 1.
 KW 3D-structure; Glycoprotein; Receptor; Signal; Transmembrane.
 FT SIGNAL 1 26
 FT CHAIN 27 551 Interleukin-2 receptor beta chain.
 FT DOMAIN 27 240 Extracellular (Potential).
 FT TRANSMEM 241 265 Potential.
 FT DOMAIN 266 551 Cytoplasmic (Potential).
 FT DOMAIN 131 229 Fibronectin type-III.
 FT SITE 220 224 WSXWS motif.
 FT SITE 278 286 Box 1 motif.
 FT DISULFID 36 46 By similarity.
 FT DISULFID 74 86 By similarity.
 FT CARBOHYD 29 29 N-linked (GlcNAc...) (Potential).
 FT CARBOHYD 43 43 N-linked (GlcNAc...) (Potential).
 FT CARBOHYD 71 71 N-linked (GlcNAc...) (Potential).
 FT CARBOHYD 149 149 N-linked (GlcNAc...) (Potential).
 FT STRAND 35 37
 FT STRAND 45 47
 FT STRAND 52 52
 FT STRAND 56 56
 FT STRAND 60 64
 FT STRAND 68 70
 FT HELIX 72 73
 FT STRAND 80 82
 FT STRAND 85 86
 FT TURN 90 92
 FT TURN 93 95
 FT STRAND 99 104
 FT STRAND 112 116
 FT STRAND 132 133
 FT STRAND 139 142
 FT STRAND 149 150
 FT STRAND 159 160
 FT TURN 163 169
 FT STRAND 178 180
 FT STRAND 185 186
 FT TURN 200 201
 FT STRAND 205 206
 FT STRAND 208 210
 FT TURN 215 216
 FT STRAND 221 221
 FT STRAND 227 228
 SQ SEQUENCE 551 AA; 61117 MW; 1A76FA1936BB7EE6 CRC64;

Query Match 9.4%; Score 278; DB 1; Length 551;
 Best Local Similarity 26.0%; Pred. No. 1.4e-10;
 Matches 137; Conservative 75; Mismatches 199; Indels 116; Gaps 31;

QY 5 WAAPLLILL--LQGGW-----GCPDLVCYTDYLTQVICILEMNLHPSTLTLTWQDQYE 56

Db 8 WRLPLLILLPLATSWAAAVNGTSQFTCFYNRANISCV---WS-----QDG 52
 QY 57 ELKDEATSCSLH---RSANAT-----HATYTCM-----DVFHMAADDIPFVNITD 100
 Db 53 ALQD--TSCQVHWPDRRRRNQTCCELLPVSQASMACNLIILGAPDSQKLTIVTVLRVLC 110
 QY 101 QSGNYSQECG--SFLLAESIKPAPPFNVTVTF--SQQYNISWRSDYEDPDPAFYMLKGLQY 156
 Db 111 REGVVRVMAIQDKPFENLRMAPISLQVVHVHETHCNISWEI---SQASHYFERHLEF 167
 QY 157 ELQVNRGDPWAVSPRKLISVDSRSVSLPLLEPRKDSSELQVRAGMPGSSVQGTWSE 216
 Db 168 EARTLSPGHTWEAP---LLTLKQKQEWICLETITPDQYEFQVRVKPLOGEF--TTWSP 222
 QY 217 WSDPVIFQTOSEELKEG---WNPHLLLLLLLVIFIPAFWSL---KTHPLRWLW-KKIW 268
 Db 223 WSQPLAPRTKPAALGKDTIPWLGHLLVGLSGAFGIILVLLINCRNTGP-----WLKKVL 278
 QY 269 A--VPSPERFFMPLYKCGSGDFKKVVGAPFTGSSLELGPWSPPEVPSTLEVYSCHPPRSPA 326
 Db 279 KCNTPDPSKFFSQLSSEHGQVQKWLSSFPSSSFSGGLAPEI-SPLEV-----L 328
 QY 327 KRLQTELOPAAELVESDGVKPKSPFWPTAONGSGSAYSEERDRPYGLVSDITVTVLDAEG 386
 Db 329 ERDKVTQL-----LLQDQKVPEA-----SLSSNHSLSCTFNQGYFFFLPDALEIEA-- 377
 QY 387 PC-----TPWCSCEDD-----GYPALDLDAGLSPGLEPDLDDAGTTVLSCGCVSAGSP 436
 Db 378 -CQVYFTYDPSYSEEDPDEGVAGAPTGSPPQLQPLSG-ED---DAYCTFSRDDLLLFSP 432
 QY 437 G-LGGP-----LGSLDLRLKPLIAD--GEDWAGGLPWGGRSPG 471
 Db 433 SLLGGPSPPTAPGSGGAGEERMPFSLQVRPRDW-DPQPLGPRPTG 478
 RESULT 6
 ID Q9Z1A0 PRELIMINARY; PRT; 890 AA.
 AC Q9Z1A0;
 DT 01-MAY-1999 (TrEMBLrel. 10, Created)
 DT 01-MAY-1999 (TrEMBLrel. 10, Last sequence update)
 DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
 DE Interleukin-5 receptor beta chain.
 GN Name=IL5;
 OS Cavia porcellus (Guinea pig).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Hystricognathi; Caviidae; Cavia.
 OX NCBI_TaxID=10141;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Logsdon N.J., Graham A., Scott C.W.;
 RL Submitted (MAR-1997) to the EMBL/GenBank/DBJ databases.
 DR EMBL; U94688; AAC77520.1; --
 DR HSSP; P32927; 1GH7.
 DR GO; GO:0016021; C:integral to membrane; IEA.
 DR GO; GO:0004907; F:interleukin receptor activity; IEA.
 DR GO; GO:0004872; F:receptor activity; IEA.
 DR GO; GO:0019221; P:cytokine and chemokine mediated signaling p...; IEA.
 DR InterPro; IPR002996; Cytnk_recept_B/G.
 DR InterPro; IPR003961; FN_III.
 DR InterPro; IPR008957; FN_III-like.
 DR InterPro; IPR00276; GPCR_Rhodpsn.
 DR InterPro; IPR003531; HemtreceptS_F1.
 DR InterPro; IPR011365; IL3recept_beta_c.
 DR Pfam; PF00041; fn3; 3.
 DR PIRSF; PIRSF001956; IL3R_beta_c; 1.
 DR SMART; SM00060; FN3; 3.
 DR PROSITE; PS0853; FN3; 2.
 DR PROSITE; PS0237; G_PROTEIN_RECP_F1; 1; UNKNOWN 1.
 DR PROSITE; PS01355; HEMATOPO_REC_S_F1; UNKNOWN 1.
 KW Receptor.
 SQ SEQUENCE 890 AA; 96578 MW; D43FB1CA88525536 CRC64;

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Query Match      8.5%; Score 250; DB 2; Length 890;
Best Local Similarity 22.7%; Pred. No. 2e-08;
Matches 150; Conservative 73; Mismatches 217; Indels 220; Gaps 36;

QY 2 PRGWAAPLALLLQGGGCP-DLVCVTDYLTQVTCILEMNLHPSTLTLTW-----51
DB 229 PSQMSPEVSWSQPDQAOQONLQCVDFGAHLSCSWEVRSQVTSVSGLYFRSLDAG 288
QY 52 -----QDQYELKDEAT--SCSLHRSAAHATHATYTHCHMDVHFHMADDIFSNITDQSG- 103
DB 289 EQECPOVQKEELHDIVTRHSCQI-RVSNRPHSQYT-----VTVRPNRGE 332
QY 104 NYSQECGSLAESIKPAPFNVTTFSCQYNISRWSDYEDPAFMYLKGKLYELOYRNR 163
DB 333 KPIRSANHIQMA-----APLTNVTKD-GDYSLRWVTE-----KMYSHIENTFEIQRTA 382
QY 164 GDPWAVSPRRKLISVDSRSVSLPLEFRKDSYELQVRAGPMPGSSYQGTWSEWSDPVIF 223
DB 383 GDRWENSKTETL--KNAHNPPLPLE--PATYILARVRVKPSGPGAYNGINSESEQRW 438
QY 224 QTSQSEELKEGMN-PHLLLLLLLVIFIP-----AFWSLKTHTPLRLMKKIWAVPSPERFF 277
DB 439 TTD-----WALPTWLVLALVIVTLALLLALRFGCLGYRLNRKWE--KIPNPSKSH 489
QY 278 M-----PLYKCGSGDFKRWG-APTGSLSLELGPWSPVPSTL 314
DB 490 LFKNGSAGLRLPDSMAFASRAPSNGVMGRFLIEGVCPADSRDSEVSLTTEDPTV 549
QY 315 EYVSHPPRSPAKRLQLTQELQPAELVESDGVKPSFWMPTAQNSGGSAYSEBERDPYGLV 374
DB 550 -----CDPSEPHSTPAASDLTQEPSPVQGPVP-----QDQFG---585
QY 375 SIDTVTVLDAEGCTWP-----CSCBDDG-----YPALDLID 405
DB 586 --DQLATDFENGYPGLPHSHSLPDLAQOQKPELGSLEYLCLPPGGAQLVLAQAT 643
QY 406 AGLSPSGLEDPLLDAGTTVLSC--GCVSAGSFG--GGPLGSLDLRLKPLADGEDWA 460
DB 644 GOAQAPAP-----ECLSGPVTQGSPLYEAGGPP-----APPASDPGSA 682
QY 461 GCLPWGGRSPGG--VSSEAGSPLAGLMDMTDFDSGFV-----GSDCSS-----P 502
DB 683 QG--PGDGPSPVILPTNSGP-----EHPVVASGYVTADLALTLSTEASSVSLAPP 735
QY 503 VECDFTS-----PGDEGP-PRSYLRQWVWIPP-----PLSSPG-PQ 536
DB 736 DLCPGLSDEAPAAPTPGKPRFGYVELPASMGPLPKSLFGFV--PPAPSPVLSFGTFQ 793

RESULT 7
ID IL2B RAT
AC P26896; STANDARD; PRT; 537 AA.
DT 01-AUG-1992 (Rel. 23, Created)
DT 01-AUG-1992 (Rel. 23, Last sequence update)
DT 05-JUL-2004 (Rel. 44, Last annotation update)
DE Interleukin-2 receptor beta chain precursor (IL-2 receptor) (P70-75)
DE (High affinity IL-2 receptor beta subunit) (CD122).
GN Name=IL2rb;
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX NCBI_TaxID=10116;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=91364784; PubMed=1889461;
RA Page T.H., Dallman M.J.;
RT "Molecular cloning of cDNAs for the rat interleukin 2 receptor alpha
RT and beta chain genes; differentially regulated gene activity in
RT response to mitogenic stimulation";
RL Eur. J. Immunol. 21:2133-2138(1991).
CC -!- FUNCTION: Receptor for interleukin 2. This beta subunit is
involved in receptor mediated endocytosis and transduces the
mitogenic signals of IL2.
SUBUNIT: Noncovalent dimer of an alpha and a beta chains. IL2R
exists in 3 different forms: a high affinity dimer, an
intermediate affinity monomer (beta chain), and a low affinity
monomer (alpha chain). The high and intermediate affinity forms
also associate with a gamma chain.
SUBCELLULAR LOCATION: Type I membrane protein.
DOMAIN: The WSXWS motif appears to be necessary for proper protein
folding and thereby efficient intracellular transport and cell-
surface receptor binding.
DOMAIN: The box 1 motif is required for JAK interaction and/or
activation.
SIMILARITY: Belongs to the type I cytokine family of receptors.
SUBFAMILY 4.
SIMILARITY: Contains 1 fibronectin type III domain.
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or send an email to license@isb-sib.ch).
EMBL; M55050; AAA41429.1; -.
HSSP; P14784; IILM.
RGD; 2896; IIL2rb.
InterPro; IPR002996; Cytokn_recept_B/G.
InterPro; IPR008957; FN_III-like_F1.
InterPro; IPR003531; Hemptrecept_F1.
PROSITE; PS00853; FN3; 1.
PROSITE; PS01355; HEMATOPO_REC_S_F1; 1.
Glycoprotein; Receptor; Signal; Transmembrane.
CHAIN 1 26
Interleukin-2 receptor beta chain.
DOMAIN 27 537
Extracellular (Potential).
TRANSMEM 27 239
Potential.
DOMAIN 240 537
Cytoplasmic (Potential).
DOMAIN 132 230
Fibronectin type-III.
SITE 221 225
WSXWS motif.
SITE 280 288
Box 1 motif.
DISULFID 36 46
By similarity.
DISULFID 74 86
By similarity.
CARBOHYD 43 43
N-linked (GlcNAc...) (Potential).
CARBOHYD 55 55
N-linked (GlcNAc...) (Potential).
CARBOHYD 71 71
N-linked (GlcNAc...) (Potential).
CARBOHYD 150 150
N-linked (GlcNAc...) (Potential).
SEQUENCE 537 AA; 60657 MW; 9C744A24F3361968 CRC64;
Query Match      8.4%; Score 248; DB 1; Length 537;
Best Local Similarity 23.6%; Pred. No. 1.4e-08;
Matches 148; Conservative 70; Mismatches 178; Indels 232; Gaps 33;
QY 5 WAAPL--LLLLLQGGW-----GCPDLVCYTDYLTQVTCILEMNLHPSTLTLTWQDQVE 56
DB 8 WRLPLYILLLLATLTVWSAAVNDGSHLCKFYNSRANVSC---MMS-----49
QY 57 ELKDEA--TSCSLHRSAAH---NAT-----HATYTCM-----DVHFHMADDIFSV 96
DB 50 --PBEALNVTSCCHHAKSDMRHWNKTCBLTPVQASMAENLILGPLDQSLTSDVLLSL 107
QY 97 NIT--DOSGNYSQBCGSLAESIKPAPFNVTTF--SGQYNISWR-----SDYEDPAFY 148
DB 108 SVVCWEKGRVVKTCFPHFDNLRLIAPHSLQVLHIETRCNISWEVSQVSHYVNP---164
QY 149 MLKGKLYELOYRNRGDPWAVSPRRKLISVDSRSVSLPLEFRK-----DSSVEL 198
DB 165 ---YLEFE-----ARRLLDRSWEDASVFLKQKQWIFLETLPDTSYEL 207
QY 199 QVRAGPMPGSSYQGTWSEWSDPVIFQTSBELKEGNPHLLLLLVIFVPAWS----254
DB 208 QRVIAORGKT--RTWSPSQPMAPRTRPADPKEIFPWLRCULLLVLCGFCFFGLSCVCV 265
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QY 57 ELKDEATSCSLHRSNAHATHATYTCMDVPH-----FMADDIPSVM 98
DB 57 -----TTCHVHAKS-NLRHWNKTCETLVRQASWACNLILGSPESQSLTSLVLDLINV 109
QY 99 T--DQSGNYSOECGSLLAESIKPAPFNVTTF--SGOYNISWR-----SDYEDPAFYML 150
DB 110 VCWEEKGWRRVKTCDPFPDNLRLVAPHSLOVLHIDTQRCNLSWKVSQVSHVIEP-----164
QY 151 KGKQYELQYRNRGDPWAVSPRRKLISVDSRSVLLPLEFRKDSSEYELQVRAGPMPGSSY 210
DB 165 ---YLEPEARRLLGHSWEDA---SVLSLKQROQWLFLMLIPSTSEYQVRVKAQRNNT- 218
QY 211 QGTWSEMSDPVIFQTO--SEELKEGWNPHLLLVIVIPAFWS-----254
DB 219 -GTWSPWSQPLTFRTPADPMKEILPMSWLRYLLLVLCGFCGFFCYVILVKRYLGPWL 277
QY 255 ---LKTHPLRWLWKKIWAVSPERFPMPLYKGCSDGFKKWGAPFTGSSLELGPMSPEVP 311
DB 278 KTVLKCH-----IPDSEFFSOLSSQHGDLQWLSPVPLSPFSFGPAPEI- 325
QY 312 STLEVYCHPPRSPAKRLQLTELQEPALVESDGVKPKFWPTAQNSGGSAYSEERDRPY 371
DB 326 SPLEVL-----GDSKAVQLL-----LLQKDSAPLPS-----PSGHSQASCFNQG 367
QY 372 -----GLVSDITVTVLDAGPCT-----WPCSCDDGY-----PA 401
DB 368 FFFHLPNALEIESCOVYTFYDPCVEEVEDGSRLEPGSPHPLPLAGEQDDYCAFP 427
QY 402 LDLDAGLEPSGLDPLDAGTT-----VLSGCVSAGSPGLGGPLGSLDLRLKPP 452
DB 428 DDL-----LFLPSLSTPNTAYGSRAPERSPLSLHGLEPLSLASRLMG-LQRP 481
QY 453 LADGEDWAGGLPWGGRSPGVSSEAGSP-----LAGLDM 488
DB 482 EGDE-----GLSANSSEAGSPVPEGNLHGQDQ 510

RESULT 9
Q8R308 PRELIMINARY; PRT; 539 AA.
AC Q8R308;
DT 01-JUN-2002 (TREMBlrel. 21, Created)
DT 01-JUN-2002 (TREMBlrel. 21, Last sequence update)
DE Interleukin 2 receptor, beta chain.
GN Name=112rb;
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RX STRAIN=CZECH II; TISSUE=Mammary tumor; DOI=10.1073/pnas.242603899;
RA Strausberg R.L., Feigold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Diachenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Donald M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahy J., Helton E., Kettman M., Madan A., Rodrigues S., Sanchez A.,
RA Whitling M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmitz J., Myers R.M., Butterfield Y.S.,
RA Krzywinski M.I., Skalska U., Smaluk D.E., Schnerch A., Schein J.E.,
RA Jones S.J., Marra M.A.
RT "Generation and initial analysis of more than 15,000 full-length human
RT and mouse cDNA sequences."
```

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RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903 (2002).
RN [2]
RP SEQUENCE FROM N.A.
RA STRAIN=CZECH II; TISSUE=Mammary tumor;
RA Strausberg R.;
RL Submitted (APR-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL; BC026869; AAH26869.1; -.
DR HSSP; P40223; ICD9.
DR MGD; MGI:96550; I12rb.
DR GO; GO:0005615; C:extracellular space; TAS.
DR GO; GO:0016021; C:integral to membrane; TAS.
DR InterPro; IPR002996; Cytokn_recept_B/G.
DR InterPro; IPR003961; FN_III.
DR InterPro; IPR008957; FN_III-like.
DR InterPro; IPR003531; Hemtrecepts_F1.
DR Pfam; PF00041; fn3; 1.
DR SMART; SM00060; FN3; 1.
DR PROSITE; PS00853; FN3; 1.
DR PROSITE; PS01355; HEMATOPO_REC_S_F1; 1.
KW Receptor.
SQ SEQUENCE 539 AA; 60556 MW; 0BB3813C68C113BB CRC64;

Query Match 8.3%; Score 245.5; DB 2; Length 539;
Best Local Similarity 23.4%; Pred. No. 2.1e-08;
Matches 137; Conservative 68; Mismatches 196; Indels 185; Gaps 29;

QY 5 WAAPL--LLLLQGGW-----GCPDLVCYTDTYLOTVICILEMWNLHPSTLTWQDOYE 56
DB 8 WSLSLVYVFLLLATPWASAAVKNCSHLECFYNSRANVSC---MWS-HEEALNV-----56
QY 57 ELKDEATSCSLHRSNAHATHATYTCMDVPH-----FMADDIPSVM 98
DB 57 -----TTCHVHAKS-NLRHWNKTCETLVRQASWACNLILGSPESQSLTSLVLDLINV 109
QY 99 T--DQSGNYSOECGSLLAESIKPAPFNVTTF--SGOYNISWR-----SDYEDPAFYML 150
DB 110 VCWEEKGWRRVKTCDPFPDNLRLVAPHSLOVLHIDTQRCNLSWKVSQVSHVIEP-----164
QY 151 KGKQYELQYRNRGDPWAVSPRRKLISVDSRSVLLPLEFRKDSSEYELQVRAGPMPGSSY 210
DB 165 ---YLEPEARRLLGHSWEDA---SVLSLKQROQWLFLMLIPSTSEYQVRVKAQRNNT- 218
QY 211 QGTWSEMSDPVIFQTO--SEELKEGWNPHLLLVIVIPAFWS-----254
DB 219 -GTWSPWSQPLTFRTPADPMKEILPMSWLRYLLLVLCGFCGFFCYVILVKRYLGPWL 277
QY 255 ---LKTHPLRWLWKKIWAVSPERFPMPLYKGCSDGFKKWGAPFTGSSLELGPMSPEVP 311
DB 278 KTVLKCH-----IPDSEFFSOLSSQHGDLQWLSPVPLSPFSFGPAPEI- 325
QY 312 STLEVYCHPPRSPAKRLQLTELQEPALVESDGVKPKFWPTAQNSGGSAYSEERDRPY 371
DB 326 SPLEVL-----GDSKAVQLL-----LLQKDSAPLPS-----PSGHSQASCFNQG 367
QY 372 -----GLVSDITVTVLDAGPCT-----WPCSCDDGY-----PA 401
DB 368 FFFHLPNALEIESCOVYTFYDPCVEEVEDGSRLEPGSPHPLPLAGEQDDYCAFP 427
QY 402 LDLDAGLEPSGLDPLDAGTT-----VLSGCVSAGS-----PGLGGPLGSLDLRL 449
DB 428 DDL-----LFLPSLSTPNTAYGSRAPERSPLSLHGLEPLSLASRLMG-LQRP 482
QY 450 KPPLADGSDWAGGLPWGGRSPGVSSEAGSP-----LAGLDM 488
DB 482 EGDE-----GLSANSSEAGSPVPEGNLHGQDQ 510

RESULT 10
Q8CBU1 PRELIMINARY; PRT; 539 AA.
AC Q8CBU1;
DT 01-MAR-2003 (TREMBlrel. 23, Created)
DT 01-MAR-2003 (TREMBlrel. 23, Last sequence update)
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RX MEDLINE=90319131; PubMed=1695379;
RA Gorman D.M., Itoh N., Kitamura T., Schreurs J., Yonehara S.,
RA Yahara I., Arai K., Miyajima A.;
RT "Cloning and expression of a gene encoding an interleukin 3 receptor-
RT like protein: identification of another member of the cytokine
RT receptor gene family.";
RL Proc. Natl. Acad. Sci. U.S.A. 87:5459-5463(1990).
CC -!- FUNCTION: High affinity receptor for interleukin-3, interleukin-5
CC and granulocyte-macrophage colony-stimulating factor.
CC -!- SUBUNIT: Heterodimer of an alpha and a beta chain. The beta chain
CC is common to the IL3, IL5 and GM-CSF receptors.
CC -!- SUBCELLULAR LOCATION: Type I membrane protein.
CC -!- DOMAIN: The WSXWS motif appears to be necessary for proper protein
CC folding and thereby efficient intracellular transport and cell-
CC surface receptor binding.
CC -!- DOMAIN: The box 1 motif is required for JAK interaction and/or
CC activation.
CC -!- SIMILARITY: Belongs to the type I cytokine family of receptors.
CC Subfamily 4.
CC -!- SIMILARITY: Contains 2 fibronectin type III domains.
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use by non-profit institutions as long as its content is in no way
CC modified and this statement is not removed. Usage by and for commercial
CC entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC or send an email to license@isb-sib.ch).
CC -----
DR EMBL; M34397; AAA37204.1; -.
DR PIR; A35782; A35782.
DR HSP; P32927; 1GH7.
DR MGD; MGI:1339759; Csf2rb1.
DR InterPro; IPR002996; Cytokn_recept_B/G.
DR InterPro; IPR000282; Cytok_receptor_2.
DR InterPro; IPR008957; FN_III-like.
DR InterPro; IPR003531; Hemtreceptors_F1.
DR PIRSF; PIRSF001956; IL3R_beta_c; 1.
DR PROSITE; PS01355; HEMATOPO_REC_S_F1; 1.
DR KW Glycoprotein; Receptor; Repeat; Signal; Transmembrane.
FT SIGNAL 1 22
FT CHAIN 23 896 Cytokine receptor common beta chain.
FT DOMAIN 23 441 Extracellular (Potential).
FT TRANSMEM 442 463 Potential.
FT DOMAIN 464 896 Cytoplasmic (Potential).
FT DOMAIN 132 241 Fibronectin type-III 1.
FT DOMAIN 343 440 Fibronectin type-III 2.
FT SITE 428 432 WSXWS motif.
FT SITE 477 485 Box 1 motif.
FT DISULFID 39 49 By similarity.
FT DISULFID 77 99 By similarity.
FT DISULFID 88 94 By similarity.
FT DISULFID 253 263 By similarity.
FT DISULFID 292 310 By similarity.
FT CARBOHYD 62 62 N-linked (GLCNAC...) (Potential).
FT CARBOHYD 141 141 N-linked (GLCNAC...) (Potential).
FT CARBOHYD 350 350 N-linked (GLCNAC...) (Potential).
SQ SEQUENCE 896 AA; 99111 MW; 8CE16EDFC07A999 CRC64;

Query Match 7.9%; Score 233; DB 1; Length 896;
Best Local Similarity 20.4%; Pred. No. 2.8e-07;
Matches 113; Conservative 86; Mismatches 220; Indels 134; Gaps 23;

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D 250 NLQCFDGIQSLHCSWEVWTTGTSVSGLYFRSPVA-----PEKCFPVKEP 299
QY 71 ANHATHATYTCMDVHFPMADIPSVNITDQSGYQECGSLLA-ESIKAPP-FNVTV 128
D 300 PGASVYTRYHCSLPPEPSAHSQVTVSVK-----HLEQGFINSYHNIQMEPTLNLTK 353
QY 129 TFSQYNISWSDVEDPAPYMLKGLQYELQYRNGDPWAVSPRKLISVDSRVSLLPL 188

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D 405 QLEPDTSYCARVRVKPI--SNYDGIWSKWSEETWKT-DWMPTLWIVLILVFLILTL 461
QY 249 IPAFWSLTKTHPLRWLWKIINAVPSPERFPMPLYKCGSDGFKKVGCAPTGSSLELGPWSP 308
D 462 ILRFGCVSVYTRYKWKKE--KIPNPSKSL-----FQDGGKGLWP----- 499
QY 309 EVPSTLEYVYCHPP--RSPAKRLQLOLQEPALVELSDGVPKPSFWPTAQNSGGSAYSEE 366
D 500 --PGSMAAFATYNALQGPQSRLLAEQ-----GESYAH 532
QY 367 RDRPYGLVSDITVTVL--DAEGPCTWPCSD--DGYPALDLDAGLESPGLEDPLLDAG 422
D 533 EDNVSPLTIEDPNIRVPPSPDTPAASESTEQLPNVQVEGTPNRPKQLPSFD-- 590
QY 423 TTVLSGCVSAGSPGLGSP-----LGSLLDRLLKPPLADGE---DWAGGLPWGSRSPG-- 472
D 591 -----FNGPYLGPQSHSLPDLQDLGSPQVGGSLKPLPAGSLAYMCLAFGGVQ 640
QY 473 -----VSESEAGSPLAGLMDTDFDSGFVGDSCSSPVCEQTSFGDGPSPRYLRQWV 525
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QY 526 IPPPLSSFGQAS 538
D 692 VTLPISSGGPEGS 704

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DT 01-JUN-2002 (TrEMBLrel. 21, Created)
DT 01-JUN-2002 (TrEMBLrel. 21, Last sequence update)
DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE Interleukin 3 receptor-like protein.
GN Name=Csf2rb1;
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
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RP SEQUENCE FROM N.A.
RC STRAIN=ILS, and ISS;
RC MEDLINE=21363810; PubMed=11471062;
RA Ehringer M.A., Thompson J., Conroy O., Xu Y., Yang F., Canniff J.,
RA Beeson M., Gordon L., Bennett B., Johnson T.E., Sikela J.M.;
RT "High-throughput sequence identification of gene coding variants
RT within alcohol-related OTUs.";
RL Mamm. Genome 12:657-663(2001).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=ILS, and ISS;
RA Ehringer M.A., Thompson J., Conroy O., Xu Y., Yang F., Canniff J.,
RA Beeson M., Gordon L., Bennett B., Johnson T.E., Sikela J.M.;
RL Submitted (FEB-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF483496; AAL90770.1; -.
DR EMBL; AF483497; AAL90771.1; -.
DR HSSP; P32927; 1GH7.
DR MGD; MGI:1339759; Csf2rb1.
DR GO; GO:0005615; C:extracellular space; TAS.
DR GO; GO:0016021; C:integral to membrane; TAS.
DR InterPro; IPR002996; Cytokn_recept_B/G.
DR InterPro; IPR000282; Cytok_receptor_2.
DR InterPro; IPR003961; FN_III.
DR InterPro; IPR008957; FN_III-like.
DR InterPro; IPR003531; Hemtreceptors_F1.
DR InterPro; IPR011365; IL3recept_beta_c.
DR Pfam; PF00041; fn3; 2.
DR PIRSF; PIRSF001956; IL3R_beta_c; 1.

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Cruaud C., Duprat S., Brottier P., Coutanceau J.-P., Gouzy J., Parra G., Lardif G., Chappie C., McKernan K.J., McEwan P., Bosak S., Kellis M., Volff J.-N., Guigs R., Zody M.C., Mesirov J., Lindblad-Toh K., Birren B., Nusbaum C., Kahn D., Robinson-Rechavi M., Laudet V., Schachter V., Quittier F., Saurin W., Scarpelli C., Wincker P., Lander E.S., Weissenbach J., Crolius H.R.; the "Analysis of the tetraodon nigroviridis genome reveals the protokaryotype of bony vertebrates and its duplication in teleost fish."

Nature 0:0-0(2004).

EMBL; AY74481; AAR25672.1; -.
GO; GO:0004872; Fireceptor activity; IEA.
InterPro; IPR02996; Cytkn_recept_B/G.
InterPro; IPR003961; FN.III.
InterPro; IPR008957; FN.III-like.
InterPro; IPR003528; HemtreceptL_F1.
Pfam; PF00041; fn3; 1.
SMART; SM00060; FN3; 1.
PROSITE; PS00853; FN3; 1.
DR PROSITE; PS01352; HEMATOP_REC_L_F1; UNKNOWN_1.
KW Receptor.

SQ SEQUENCE 529 AA; 59609 MW; C4A04BFC94E9C3B6 CRC64;

Db 278 WSDMTECLADGNT-----TDLCR---FQVHSGKFKVKLSRDKSPLSSTTFY 320
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Qy 164 G-DPAVSPRRKLISVDSRSVSL---LPLEFRKSSYELQVRAGFMPGSSYQGTWSEWS 219
Db 372 GTDWTI-----LSIQSAETSTCVQLPLGIH-----YRAKIRAKP-DGITYSGDMSDSD 420
Qy 220 PVIFOTQSEELKEGNPHLL---LLLIVIFIPAFWSLKTPLWRLWKI-W-AVPSPER 275
Db 421 VITGTPADK-----STELLICIPICMLVIAVITISLPKTFSLKLY--FWPPVPNPDX 473
Qy 276 FFMPLYKCSGDFKXWVGAPFTGSSLELGPSPV-----STLEVYSCHPPRSAPKR 328
Db 474 VLQGYLTENG--QRW-----NPMLTTPKCLEIDIAAGFLEVMSEDEAVVSEKR 519
Qy 329 LQL-TELQPAELVESDGVKPSFWPTAQNSGGSAyseERDRPYGLVSDITVTILD---- 383
Db 520 SKTSTQL-----LSAEQRLPRPE--PPDPPGGEAYS-----GYVTLRKGTFIHNIST 565
Qy 384 ---AEGPCTWPC--SCEDDGYPALDLADG-----LESPGLEDPLL---DAGT 423
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Qy 424 TVLSCGC 430
Db 624 LYTNLPC 630

Search completed: July 9, 2005, 11:47:03
Job time : 181 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: July 9, 2005, 11:38:30 ; Search time 42 Seconds
(without alignments)
956.219 Million cell updates/sec

Title: US-10-620-169-4
Perfect score: 2958
Sequence: 1 MPRGWAAPLLLLLQGGWGC.....YLRQWVPPPLSSFPQAS 538

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 513545 seqs, 74649064 residues

Total number of hits satisfying chosen parameters: 513545

Minimum DB seq length: 0
Maximum DB seq length: 2000000000
Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Issued Patents AA: *
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2: /cgn2_6/prodata/1/iaa/5B COMB.pep: *
3: /cgn2_6/prodata/1/iaa/6A COMB.pep: *
4: /cgn2_6/prodata/1/iaa/6B COMB.pep: *
5: /cgn2_6/prodata/1/iaa/PCTUS COMB.pep: *
6: /cgn2_6/prodata/1/iaa/backfiles1.pep: *

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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1	2958	100.0	538	3	US-09-040-005-2
2	2958	100.0	538	3	US-09-522-217-115
3	2958	100.0	538	4	US-09-404-641-2
4	2958	100.0	538	4	US-09-923-246-115
5	2958	100.0	538	4	US-10-295-723-115
6	2958	100.0	538	4	US-10-414-186-2
7	2958	100.0	538	4	US-09-825-561A-2
8	2958	100.0	538	4	US-10-243-072-2
9	2958	100.0	547	4	US-09-949-016-11544
10	2817	95.2	568	4	US-09-825-561A-65
11	1735.5	58.7	529	4	US-09-404-641-85
12	1735.5	58.7	529	4	US-10-414-186-85
13	1735.5	58.7	529	4	US-09-825-561A-12
14	1735.5	58.7	529	4	US-10-243-072-85
15	1729.5	58.5	529	4	US-09-732-234-6
16	1729.5	58.5	529	4	US-09-784-859-6
17	1302	44.0	567	4	US-09-825-561A-16
18	1221.5	41.3	397	4	US-10-404-641-81
19	1221.5	41.3	397	4	US-10-414-186-81
20	1221.5	41.3	397	4	US-10-243-072-81
21	1197	40.5	606	3	US-09-522-217-97
22	1197	40.5	606	4	US-09-404-641-51
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24	1197	40.5	606	4	US-10-295-723-97
25	1197	40.5	606	4	US-10-414-186-51
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29 1135 38.4 261 4 US-09-825-561A-71
30 1100 37.2 247 4 US-09-825-561A-69
31 844 28.5 486 4 US-09-825-561A-73
32 677.5 22.9 240 4 US-09-404-641-70
33 677.5 22.9 240 4 US-10-414-186-70
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38 278 9.4 551 6 5198359-2
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41 248.5 8.4 539 6 549756-4
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44 231 7.8 536 4 US-09-949-016-8560
45 220.5 7.5 468 1 US-08-164-614A-7

ALIGNMENTS

RESULT 1

US-09-040-005-2
; Sequence 2, Application US/09040005
; Patent No. 6057128
; GENERAL INFORMATION:
; APPLICANT: Donaldson, Debra
; APPLICANT: Unger, Michelle
; TITLE OF INVENTION: MU-1 RECEPTOR
; NUMBER OF SEQUENCES: 8
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Genetics Institute, Inc.
; STREET: 87 Cambridgepark Drive
; CITY: Cambridge
; STATE: MA
; COUNTRY: USA
; ZIP: 02140
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/040,005
; FILING DATE:
; CLASSIFICATION:
; ATTORNEY/AGENT INFORMATION:
; NAME: Brown, Scott A
; REGISTRATION NUMBER: 32,724
; REFERENCE/DOCKET NUMBER: G15320
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 617-498-8224
; TELEFAX: 617-876-5851
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 538 amino acids
; TYPE: amino acid
; STRANDEDNESS:
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-09-040-005-2

Query Match 100.0%; Score 2958; DB 3; Length 538;

Best Local Similarity 100.0%; Pred. No. 3e-266;
Matches 538; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db 61 EATSCSLHRSAHNATHATYTCMDVFFHFMADDIFSVNITDQSGNYSCQSGFLLAESIKP 120
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RESULT 2

US-09-522-217-115
; Sequence 115, Application US/09522217
; Patent No. 6307024
; GENERAL INFORMATION:
; APPLICANT: Presnell, Scott R.
; APPLICANT: Sprecher, Cindy A.
; APPLICANT: Foster, Donald D.
; APPLICANT: Holly, Richard D.
; APPLICANT: Gross, Jane A.
; APPLICANT: Johnston, Janet V.
; APPLICANT: Nelson, Andrew J.
; APPLICANT: Dillon, Stacey R.
; APPLICANT: Hammond, Angela K.
; TITLE OF INVENTION: NOVEL CYTOKINE ZALPHA11 LIGAND
; FILE REFERENCE: 99-16
; CURRENT APPLICATION NUMBER: US/09/522,217
; EARLIER FILING DATE: 2000-03-09
; EARLIER APPLICATION NUMBER: US 60/123,547
; EARLIER FILING DATE: 1999-03-09
; EARLIER APPLICATION NUMBER: US 60/123,904
; EARLIER FILING DATE: 1999-03-11
; EARLIER APPLICATION NUMBER: US 60/142,013
; EARLIER FILING DATE: 1999-07-01
; NUMBER OF SEQ ID NOS: 115
; SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 115
; LENGTH: 538
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-522-217-115

Query Match 100.0%; Score 2958; DB 3; Length 538;
Best Local Similarity 100.0%; Pred. No. 3e-266;
Matches 538; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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RESULT 3

US-09-404-641-2
; Sequence 2, Application US/09404641
; Patent No. 6576744
; GENERAL INFORMATION:
; APPLICANT: Presnell, Scott R.
; APPLICANT: Conklin, Darrell C.
; APPLICANT: No. 6576744ak, Julia E.
; APPLICANT: Hammond, Angela K.
; TITLE OF INVENTION: CYTOKINE RECEPTOR ZAPLH11
; FILE REFERENCE: 98-55
; CURRENT APPLICATION NUMBER: US/09/404,641
; EARLIER FILING DATE: 1999-09-23
; EARLIER APPLICATION NUMBER: US 60/100,896
; EARLIER FILING DATE: 1998-09-23
; EARLIER APPLICATION NUMBER: US 60/123,546
; EARLIER FILING DATE: 1999-03-09
; EARLIER APPLICATION NUMBER: US 60/142,574
; EARLIER FILING DATE: 1999-07-06
; NUMBER OF SEQ ID NOS: 91
; SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 2
; LENGTH: 538
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-404-641-2

Query Match 100.0%; Score 2958; DB 4; Length 538;
Best Local Similarity 100.0%; Pred. No. 3e-266;
Matches 538; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db 1 MPRGWAAPLLLLLLQGGGCPDLVCYTDYLTQTVICILEMNLHPSTLTLTWQDQYEELKD 60
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RESULT 4

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; Sequence 115, Application US/09923246
; Patent No. 6605272
; GENERAL INFORMATION:
; APPLICANT: No. 6605272ak, Julia E.
; APPLICANT: Preenell, Scott R.
; APPLICANT: Sprecher, Cindy A.
; APPLICANT: Foster, Donald C.
; APPLICANT: Holly, Richard D.
; APPLICANT: Gross, Jane A.
; APPLICANT: Johnston, Janet V.
; APPLICANT: Nelson, Andrew J.
; APPLICANT: Dillon, Stacey R.
; APPLICANT: Hammond, Angela K.
; TITLE OF INVENTION: NOVEL CYTOKINE ZALPHA11 LIGAND
; FILE REFERENCE: 99-16
; CURRENT APPLICATION NUMBER: US/09/923,246
; CURRENT FILING DATE: 2001-08-03
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: US/09/522,217
; PRIOR FILING DATE: EARLIER FILING DATE: 2000-03-09
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: US 60/123,904
; PRIOR FILING DATE: EARLIER FILING DATE: 1999-03-11
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: US 60/142,013
; PRIOR FILING DATE: EARLIER FILING DATE: 1999-07-01
; NUMBER OF SEQ ID NOS: 115
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 115
; LENGTH: 538
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-923-246-115
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Query Match 100.0%; Score 2958; DB 4; Length 538;
Best Local Similarity 100.0%; Pred. No. 3e-266;
Matches 538; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MPRGWAAPLLLLLQGGWCPDLVCYTDYLTQVICILEMNLHPSTLTLTWQDQYEELKD 60
Db 1 MPRGWAAPLLLLLQGGWCPDLVCYTDYLTQVICILEMNLHPSTLTLTWQDQYEELKD 60

Qy 61 EATSCSLHRSANATHATYTCMDVHFWMADDIFSVNITDQSGNYSQCGSFLAESIKP 120
Db 61 EATSCSLHRSANATHATYTCMDVHFWMADDIFSVNITDQSGNYSQCGSFLAESIKP 120
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Qy 121 APPFNVTTFSGQYNIWSRSDYEDPAFYMLKGLQYELQYRNRGDPWAVSPRRKLISVDS 180
Db 121 APPFNVTTFSGQYNIWSRSDYEDPAFYMLKGLQYELQYRNRGDPWAVSPRRKLISVDS 180
Qy 181 RVSLLPLLEFRKDSSEYELQVRAGMPGSSYQGTWSEWSDPVIQTQSEBELKEGWNPHLL 240
Db 181 RVSLLPLLEFRKDSSEYELQVRAGMPGSSYQGTWSEWSDPVIQTQSEBELKEGWNPHLL 240
Qy 241 LLLLVIVIPAFWSLTKTHPLWRLWKKIWAIVSPERFPMPLYKGCSDGDFKMWGAPFTGSS 300
Db 241 LLLLVIVIPAFWSLTKTHPLWRLWKKIWAIVSPERFPMPLYKGCSDGDFKMWGAPFTGSS 300
Qy 301 LELGWSPEVSTLEVISCHPPRSPAKRLQLTELQEPALVESDGVKPSFWMPTAQNCGG 360
Db 301 LELGWSPEVSTLEVISCHPPRSPAKRLQLTELQEPALVESDGVKPSFWMPTAQNCGG 360
Qy 361 SAYSEERDRPYGLVSDITVTVLDAEGPCTWPCSCDDGYPALDLDAGLEPSPGLDPLLD 420
Db 361 SAYSEERDRPYGLVSDITVTVLDAEGPCTWPCSCDDGYPALDLDAGLEPSPGLDPLLD 420
Qy 421 AGTTVLSCGCVSAGSPGLGGLSLDLRLKPLADGEDWAGGLPWGGRSPGVSSEAGS 480
Db 421 AGTTVLSCGCVSAGSPGLGGLSLDLRLKPLADGEDWAGGLPWGGRSPGVSSEAGS 480
Qy 481 PLAGLDMDTFDSGFVSGDCSSPVECDFTSPGDEGPPRSYLRQWVIPPPLSSPGQAS 538
Db 481 PLAGLDMDTFDSGFVSGDCSSPVECDFTSPGDEGPPRSYLRQWVIPPPLSSPGQAS 538
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RESULT 5

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US-10-295-723-115
; Sequence 115, Application US/10295723
; Patent No. 6686178
; GENERAL INFORMATION:
; APPLICANT: No. 6686178ak, Julia E.
; APPLICANT: Preenell, Scott R.
; APPLICANT: Sprecher, Cindy A.
; APPLICANT: Foster, Donald C.
; APPLICANT: Holly, Richard D.
; APPLICANT: Gross, Jane A.
; APPLICANT: Johnston, Janet V.
; APPLICANT: Nelson, Andrew J.
; APPLICANT: Dillon, Stacey R.
; APPLICANT: Hammond, Angela K.
; TITLE OF INVENTION: NOVEL CYTOKINE ZALPHA11 LIGAND
; FILE REFERENCE: 99-16
; CURRENT APPLICATION NUMBER: US/10/295,723
; CURRENT FILING DATE: 2002-11-15
; PRIOR APPLICATION NUMBER: 09/522,217
; PRIOR FILING DATE: 2000-03-09
; PRIOR APPLICATION NUMBER: US 60/123,547
; PRIOR FILING DATE: 1999-03-09
; PRIOR APPLICATION NUMBER: US 60/123,904
; PRIOR FILING DATE: 1999-03-11
; PRIOR APPLICATION NUMBER: US 60/142,013
; PRIOR FILING DATE: 1999-07-01
; NUMBER OF SEQ ID NOS: 115
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 115
; LENGTH: 538
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-295-723-115
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Query Match 100.0%; Score 2958; DB 4; Length 538;
Best Local Similarity 100.0%; Pred. No. 3e-266;
Matches 538; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MPRGWAAPLLLLLQGGWCPDLVCYTDYLTQVICILEMNLHPSTLTLTWQDQYEELKD 60
Db 1 MPRGWAAPLLLLLQGGWCPDLVCYTDYLTQVICILEMNLHPSTLTLTWQDQYEELKD 60

Qy 61 EATSCSLHRSANATHATYTCMDVHFWMADDIFSVNITDQSGNYSQCGSFLAESIKP 120
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Db 61 EATCSLHSAHNATHATYTCMDVHFHMADDIFSUNITDQSGYSCGSGFLAESTKP 120
Qy 121 APPENVVTFSGQYNI SWRSYEDPAFYMLKGKQLQYELQYRNRGDPWAVSPRRKLI SVDS 180
Db 121 APPENVVTFSGQYNI SWRSYEDPAFYMLKGKQLQYELQYRNRGDPWAVSPRRKLI SVDS 180
Qy 181 RSVSLLPLEFRKDSYELQVRAGMPGSSYOGTWSEWSDPVI FOTQSEELKEGWNPHLLL 240
Db 181 RSVSLLPLEFRKDSYELQVRAGMPGSSYOGTWSEWSDPVI FOTQSEELKEGWNPHLLL 240
Qy 241 LLLLVIVIFAFWLSKTHPLWRLWKKI WAVSPERFFMPLYKGCSDGDFKMWGAPFTGSS 300
Db 241 LLLLVIVIFAFWLSKTHPLWRLWKKI WAVSPERFFMPLYKGCSDGDFKMWGAPFTGSS 300
Qy 301 LELGWSPEVSTLEVYSCHPSPRPAKRLQLTQLQEPALVESDGVKPKSFWPTAQNSSG 360
Db 301 LELGWSPEVSTLEVYSCHPSPRPAKRLQLTQLQEPALVESDGVKPKSFWPTAQNSSG 360
Qy 361 SAYSEERDRPYGLVSI DTVTVLDAEGPCTWPCSCDDGYPALDLDAGLESPGLEDPILLD 420
Db 361 SAYSEERDRPYGLVSI DTVTVLDAEGPCTWPCSCDDGYPALDLDAGLESPGLEDPILLD 420
Qy 421 AGTTVLSGCVSAGSPGLGGPLGSLDLRLKPLADGEDWAGGLPWGGRSPGCVSESEAGS 480
Db 421 AGTTVLSGCVSAGSPGLGGPLGSLDLRLKPLADGEDWAGGLPWGGRSPGCVSESEAGS 480
Qy 481 PLAGLDMDTFDSGFVSGDCSPVECDFTSPGDEGPPRSYLRQWVIPPPLSSPGFQAS 538
Db 481 PLAGLDMDTFDSGFVSGDCSPVECDFTSPGDEGPPRSYLRQWVIPPPLSSPGFQAS 538

RESULT 6

US-10-414-186-2
; Sequence 2, Application US/10414186
; Patent No. 6692924
; GENERAL INFORMATION:
; APPLICANT: Presnell, Scott R.
; APPLICANT: Conklin, Darrell C.
; APPLICANT: No. 6692924ak, Julia E.
; APPLICANT: Hammond, Angela K.
; TITLE OF INVENTION: CYTOKINE RECEPTOR ZAPLHALL
; FILE REFERENCE: 98-55
; CURRENT APPLICATION NUMBER: US/10/414,186
; CURRENT FILING DATE: 2003-04-14
; PRIOR APPLICATION NUMBER: US/09/404,641
; PRIOR FILING DATE: 1999-09-23
; PRIOR FILING DATE: EARLIER FILING DATE: 1998-09-23
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: US 60/100,896
; PRIOR FILING DATE: EARLIER FILING DATE: 1999-03-09
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: US 60/142,574
; PRIOR FILING DATE: EARLIER FILING DATE: 1999-07-06
; NUMBER OF SEQ ID NOS: 91
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 2
; LENGTH: 538
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-414-186-2

Query Match 100.0%; Score 2958; DB 4; Length 538;
Best Local Similarity 100.0%; Pred. No. 3e-266;
Matches 538; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MPRGWAAPLLLLLQGGWGPCDLVCYTDYLTQTVICILEMNLHPSTLTLTWQDQVEELKD 60
Db 1 MPRGWAAPLLLLLQGGWGPCDLVCYTDYLTQTVICILEMNLHPSTLTLTWQDQVEELKD 60
Qy 61 EATCSLHSAHNATHATYTCMDVHFHMADDIFSUNITDQSGYSCGSGFLAESTKP 120
Db 61 EATCSLHSAHNATHATYTCMDVHFHMADDIFSUNITDQSGYSCGSGFLAESTKP 120

Qy 121 APPENVVTFSGQYNI SWRSYEDPAFYMLKGKQLQYELQYRNRGDPWAVSPRRKLI SVDS 180
Db 121 APPENVVTFSGQYNI SWRSYEDPAFYMLKGKQLQYELQYRNRGDPWAVSPRRKLI SVDS 180
Qy 181 RSVSLLPLEFRKDSYELQVRAGMPGSSYOGTWSEWSDPVI FOTQSEELKEGWNPHLLL 240
Db 181 RSVSLLPLEFRKDSYELQVRAGMPGSSYOGTWSEWSDPVI FOTQSEELKEGWNPHLLL 240
Qy 241 LLLLVIVIFAFWLSKTHPLWRLWKKI WAVSPERFFMPLYKGCSDGDFKMWGAPFTGSS 300
Db 241 LLLLVIVIFAFWLSKTHPLWRLWKKI WAVSPERFFMPLYKGCSDGDFKMWGAPFTGSS 300
Qy 301 LELGWSPEVSTLEVYSCHPSPRPAKRLQLTQLQEPALVESDGVKPKSFWPTAQNSSG 360
Db 301 LELGWSPEVSTLEVYSCHPSPRPAKRLQLTQLQEPALVESDGVKPKSFWPTAQNSSG 360
Qy 361 SAYSEERDRPYGLVSI DTVTVLDAEGPCTWPCSCDDGYPALDLDAGLESPGLEDPILLD 420
Db 361 SAYSEERDRPYGLVSI DTVTVLDAEGPCTWPCSCDDGYPALDLDAGLESPGLEDPILLD 420
Qy 421 AGTTVLSGCVSAGSPGLGGPLGSLDLRLKPLADGEDWAGGLPWGGRSPGCVSESEAGS 480
Db 421 AGTTVLSGCVSAGSPGLGGPLGSLDLRLKPLADGEDWAGGLPWGGRSPGCVSESEAGS 480
Qy 481 PLAGLDMDTFDSGFVSGDCSPVECDFTSPGDEGPPRSYLRQWVIPPPLSSPGFQAS 538
Db 481 PLAGLDMDTFDSGFVSGDCSPVECDFTSPGDEGPPRSYLRQWVIPPPLSSPGFQAS 538

RESULT 7

US-09-825-561A-2
; Sequence 2, Application US/09825561A
; Patent No. 6777539
; GENERAL INFORMATION:
; APPLICANT: Sprecher, Cindy A.
; APPLICANT: No. 6777539ak, Julia E.
; APPLICANT: West, James W.
; APPLICANT: Presnell, Scott R.
; APPLICANT: Holly, Richard D.
; APPLICANT: Nelson, Andrew J.
; TITLE OF INVENTION: SOLUBLE ZAPLHALL CYTOKINE RECEPTORS
; FILE REFERENCE: 00-22
; CURRENT APPLICATION NUMBER: US/09/825,561A
; CURRENT FILING DATE: 2000-04-05
; PRIOR APPLICATION NUMBER: US 60/194,731
; PRIOR FILING DATE: 2000-04-05
; PRIOR APPLICATION NUMBER: US 60/222,121
; PRIOR FILING DATE: 2000-07-28
; NUMBER OF SEQ ID NOS: 86
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 2
; LENGTH: 538
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-825-561A-2

Query Match 100.0%; Score 2958; DB 4; Length 538;
Best Local Similarity 100.0%; Pred. No. 3e-266;
Matches 538; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MPRGWAAPLLLLLQGGWGPCDLVCYTDYLTQTVICILEMNLHPSTLTLTWQDQVEELKD 60
Db 1 MPRGWAAPLLLLLQGGWGPCDLVCYTDYLTQTVICILEMNLHPSTLTLTWQDQVEELKD 60
Qy 61 EATCSLHSAHNATHATYTCMDVHFHMADDIFSUNITDQSGYSCGSGFLAESTKP 120
Db 61 EATCSLHSAHNATHATYTCMDVHFHMADDIFSUNITDQSGYSCGSGFLAESTKP 120
Qy 121 APPENVVTFSGQYNI SWRSYEDPAFYMLKGKQLQYELQYRNRGDPWAVSPRRKLI SVDS 180
Db 121 APPENVVTFSGQYNI SWRSYEDPAFYMLKGKQLQYELQYRNRGDPWAVSPRRKLI SVDS 180
Qy 181 RSVSLLPLEFRKDSYELQVRAGMPGSSYOGTWSEWSDPVI FOTQSEELKEGWNPHLLL 240


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Db 181 RSVSLLPLEFRKDSSEYELQVRAGMPGSSYQGTWSESDPVI FQTQSEBELKEGWNPHLLL 240
Qy 241 LLLLVIVFIPAFWSLTKTHPLWRLWKKIWA VPSPERFFMPLYKGCSDGDFKWKVGAFTGSS 300
Db 241 LLLLVIVFIPAFWSLTKTHPLWRLWKKIWA VPSPERFFMPLYKGCSDGDFKWKVGAFTGSS 300
Qy 301 LELGWSPEVSTLEVYSCHPSPRPAKRLQ LTELQEPALVESDGVKPSFWPTAQNCGG 360
Db 301 LELGWSPEVSTLEVYSCHPSPRPAKRLQ LTELQEPALVESDGVKPSFWPTAQNCGG 360
Qy 361 SAYSEERDRPYGLVSIIDTVTLDAEGPCT WPCSCDDGYPALDLDAGLEPSPGLSDPLLD 420
Db 361 SAYSEERDRPYGLVSIIDTVTLDAEGPCT WPCSCDDGYPALDLDAGLEPSPGLSDPLLD 420
Qy 421 AGTTVLSGCCVSAGSPGLGGPLGSLLDRL KPLADGEDWAGGLPWGGRSPGVSSEAGS 480
Db 421 AGTTVLSGCCVSAGSPGLGGPLGSLLDRL KPLADGEDWAGGLPWGGRSPGVSSEAGS 480
Qy 481 PLAGLDMDTDFSGFVSGDCSSPVECDFTS PGDEGPPRSYLRQWVVI PPLSPGPQAS 538
Db 481 PLAGLDMDTDFSGFVSGDCSSPVECDFTS PGDEGPPRSYLRQWVVI PPLSPGPQAS 538
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RESULT 8

US-10-243-072-2

; Sequence 2, Application US/10243072

; Patent No. 6803451

; GENERAL INFORMATION:

; APPLICANT: Prenelli, Scott R.

; APPLICANT: Conklin, Darrell C.

; APPLICANT: No. 6803451ak, Julia E.

; APPLICANT: Hammond, Angela K.

; TITLE OF INVENTION: CYTOKINE RECEPTOR ZAPLHA11

; FILE REFERENCE: 98-55C1

; CURRENT APPLICATION NUMBER: US/10/243,072

; CURRENT FILING DATE: 2002-09-13

; PRIOR APPLICATION NUMBER: 09/628,127

; PRIOR FILING DATE: 2000-07-28

; PRIOR APPLICATION NUMBER: US 60/100,896

; PRIOR FILING DATE: 1998-09-23

; PRIOR APPLICATION NUMBER: US 60/123,546

; PRIOR FILING DATE: 1999-03-09

; PRIOR APPLICATION NUMBER: US 60/142,574

; PRIOR FILING DATE: 1999-07-06

; PRIOR APPLICATION NUMBER: US 09/404,641

; PRIOR FILING DATE: 1999-09-23

; NUMBER OF SEQ ID NOS: 92

; SOFTWARE: FastSeq for Windows Version 3.0

; SEQ ID NO 2

; LENGTH: 538

; TYPE: PRT

; ORGANISM: Homo sapiens

US-10-243-072-2

Query Match 100.0%; Score 2958; DB 4; Length 538;

Best Local Similarity 100.0%; Pred. No. 3e-266;

Matches 538; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy 1 MPRGWAAPLLLLLQGGWGCPLVCYTDYLTQTVICILEMNNLHPSTLTLTWQDOYEELKD 60
Db 1 MPRGWAAPLLLLLQGGWGCPLVCYTDYLTQTVICILEMNNLHPSTLTLTWQDOYEELKD 60
Qy 61 EATCSLHRSAHNATHATYTTCHMDVHFHMADDIFSVNITDQSGNYSCQSGFLLAESIKP 120
Db 61 EATCSLHRSAHNATHATYTTCHMDVHFHMADDIFSVNITDQSGNYSCQSGFLLAESIKP 120
Qy 121 APPNVNVTTFSGQYNISWRSDYEDPAFYMLKGKQLQYELQYRNRPDPAVSPRRKLISVDS 180
Db 121 APPNVNVTTFSGQYNISWRSDYEDPAFYMLKGKQLQYELQYRNRPDPAVSPRRKLISVDS 180
Qy 181 RSVSLLPLEFRKDSSEYELQVRAGMPGSSYQGTWSESDPVI FQTQSEBELKEGWNPHLLL 240
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Db 181 RSVSLLPLEFRKDSSEYELQVRAGMPGSSYQGTWSESDPVI FQTQSEBELKEGWNPHLLL 240
Qy 241 LLLLVIVFIPAFWSLTKTHPLWRLWKKIWA VPSPERFFMPLYKGCSDGDFKWKVGAFTGSS 300
Db 241 LLLLVIVFIPAFWSLTKTHPLWRLWKKIWA VPSPERFFMPLYKGCSDGDFKWKVGAFTGSS 300
Qy 301 LELGWSPEVSTLEVYSCHPSPRPAKRLQ LTELQEPALVESDGVKPSFWPTAQNCGG 360
Db 301 LELGWSPEVSTLEVYSCHPSPRPAKRLQ LTELQEPALVESDGVKPSFWPTAQNCGG 360
Qy 361 SAYSEERDRPYGLVSIIDTVTLDAEGPCT WPCSCDDGYPALDLDAGLEPSPGLSDPLLD 420
Db 361 SAYSEERDRPYGLVSIIDTVTLDAEGPCT WPCSCDDGYPALDLDAGLEPSPGLSDPLLD 420
Qy 421 AGTTVLSGCCVSAGSPGLGGPLGSLLDRL KPLADGEDWAGGLPWGGRSPGVSSEAGS 480
Db 421 AGTTVLSGCCVSAGSPGLGGPLGSLLDRL KPLADGEDWAGGLPWGGRSPGVSSEAGS 480
Qy 481 PLAGLDMDTDFSGFVSGDCSSPVECDFTS PGDEGPPRSYLRQWVVI PPLSPGPQAS 538
Db 481 PLAGLDMDTDFSGFVSGDCSSPVECDFTS PGDEGPPRSYLRQWVVI PPLSPGPQAS 538
```

RESULT 9

US-09-949-016-11544

; Sequence 11544, Application US/09949016

; Patent No. 6812339

; GENERAL INFORMATION:

; APPLICANT: VENTER, J. Craig et al.

; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED

; TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF

; FILE REFERENCE: CLO01307

; CURRENT APPLICATION NUMBER: US/09/949,016

; CURRENT FILING DATE: 2000-04-14

; PRIOR APPLICATION NUMBER: 60/241,755

; PRIOR FILING DATE: 2000-10-20

; PRIOR APPLICATION NUMBER: 60/237,768

; PRIOR FILING DATE: 2000-10-03

; PRIOR APPLICATION NUMBER: 60/231,498

; PRIOR FILING DATE: 2000-09-08

; NUMBER OF SEQ ID NOS: 207012

; SOFTWARE: FastSeq for Windows Version 4.0

; SEQ ID NO 11544

; LENGTH: 547

; TYPE: PRT

; ORGANISM: Human

US-09-949-016-11544

Query Match 100.0%; Score 2958; DB 4; Length 547;

Best Local Similarity 100.0%; Pred. No. 3.1e-266;

Matches 538; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy 1 MPRGWAAPLLLLLQGGWGCPLVCYTDYLTQTVICILEMNNLHPSTLTLTWQDOYEELKD 60
Db 10 MPRGWAAPLLLLLQGGWGCPLVCYTDYLTQTVICILEMNNLHPSTLTLTWQDOYEELKD 69
Qy 61 EATCSLHRSAHNATHATYTTCHMDVHFHMADDIFSVNITDQSGNYSCQSGFLLAESIKP 120
Db 70 EATCSLHRSAHNATHATYTTCHMDVHFHMADDIFSVNITDQSGNYSCQSGFLLAESIKP 129
Qy 121 APPNVNVTTFSGQYNISWRSDYEDPAFYMLKGKQLQYELQYRNRPDPAVSPRRKLISVDS 180
Db 130 APPNVNVTTFSGQYNISWRSDYEDPAFYMLKGKQLQYELQYRNRPDPAVSPRRKLISVDS 189
Qy 181 RSVSLLPLEFRKDSSEYELQVRAGMPGSSYQGTWSESDPVI FQTQSEBELKEGWNPHLLL 240
Db 190 RSVSLLPLEFRKDSSEYELQVRAGMPGSSYQGTWSESDPVI FQTQSEBELKEGWNPHLLL 249
Qy 241 LLLLVIVFIPAFWSLTKTHPLWRLWKKIWA VPSPERFFMPLYKGCSDGDFKWKVGAFTGSS 300
Db 250 LLLLVIVFIPAFWSLTKTHPLWRLWKKIWA VPSPERFFMPLYKGCSDGDFKWKVGAFTGSS 309
Qy 301 LELGWSPEVSTLEVYSCHPSPRPAKRLQ LTELQEPALVESDGVKPSFWPTAQNCGG 360
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Db 310 LELGPMSEVSTLEVSCHPRSPAKRLQLTELQEPALVESDGVKPSFWPMTAQNQSGG 369
Qy 361 SAYSEERDRPYGLVSIIDVTVLDAEGPCTWPCSCEDDGYPALDLDAGLESPGLEDDPLLD 420
Db 370 SAYSEERDRPYGLVSIIDVTVLDAEGPCTWPCSCEDDGYPALDLDAGLESPGLEDDPLLD 429
Qy 421 AGTTVLSCGCVSAGSPGLGGPLGSLLDRLKPLADGEDWAGGLPWGGRSPGGVSESEAGS 480
Db 430 AGTTVLSCGCVSAGSPGLGGPLGSLLDRLKPLADGEDWAGGLPWGGRSPGGVSESEAGS 489
Qy 481 PLAGLDMDTFDSGFGVSCSPVECDFTSPGDEGPPRSYLRQWVIPPPLSSPGPQAS 538
Db 490 PLAGLDMDTFDSGFGVSCSPVECDFTSPGDEGPPRSYLRQWVIPPPLSSPGPQAS 547

RESULT 10

US-09-825-561A-65
; Sequence 65, Application US/09825561A
; Patent No. 6777539
; GENERAL INFORMATION:
; APPLICANT: Sprecher, Cindy A.
; APPLICANT: No. 6777539ak, Julia E.
; APPLICANT: West, James W.
; APPLICANT: Presnell, Scott R.
; APPLICANT: Holly, Richard D.
; APPLICANT: Nelson, Andrew J.
; TITLE OF INVENTION: SOLUBLE ZAPLPHALL CYTOKINE RECEPTORS
; FILE REFERENCE: 00-22
; CURRENT APPLICATION NUMBER: US/09/825,561A
; PRIOR FILING DATE: 2000-04-05
; PRIOR APPLICATION NUMBER: US 60/194,731
; PRIOR FILING DATE: 2000-04-05
; PRIOR APPLICATION NUMBER: US 60/222,121
; PRIOR FILING DATE: 2000-07-28
; NUMBER OF SEQ ID NOS: 86
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 65
; LENGTH: 568
; TYPE: PRT
; ORGANISM: homo sapiens
US-09-825-561A-65

Query Match 95.2%; Score 2817; DB 4; Length 568;
Best Local Similarity 89.9%; Pred. No. 4.3e-253;
Matches 523; Conservative 0; Mismatches 1; Indels 58; Gaps 3;
Qy 1 MPRGWAAPLLLLLQGG-----GMGCPDLVCYTDYLTQVI 34
Db 1 MPRGWAAPLLLLLQGGALGEMERKLCSPKPPPTKASLPDTPPGMGCPDLVCYTDYLTQVI 60
Qy 35 CILEMNNLHPSTLTWTW-----ODQYEELKDBATSCSLHRSNAHATH 76
Db 61 CILEMNNLHPSTLTWTWLSNNTGCIKDRTLDLRQDQYEELKDBATSCSLHRSNAHATH 120
Qy 77 ATYTCHMDVHFHMADDI FSVNITDQSGNYSCGSLAEISIKPAPPENVTVTSGQYNI 136
Db 121 ATYTCHMDVHFHMADDI FSVNITDQSGNYSCGSLAE-----SRQYNI 166
Qy 137 SWRSYEDPAPFYMKGKQYELQYLRNRPDPAWSPRRKLI SVDSRSVSLLLPLEPRKDSY 196
Db 167 SWRSYEDPAPFYMKGKQYELQYLRNRPDPAWSPRRKLI SVDSRSVSLLLPLEPRKDSY 226
Qy 197 ELQVRAGMPGSSYOGTWSWSDPVI FQTSBELKEGNPHLLLLLLLVIIPAFWLSK 256
Db 227 ELQVRAGMPGSSYOGTWSWSDPVI FQTSBELKEGNPHLLLLLLLVIIPAFWLSK 286
Qy 257 THPLWRLWKKIWAVSPERFPMPLVKGCGDPKWWGAPFTGSSLELGPWSPVSTLEV 316
Db 287 THPLWRLWKKIWAVSPERFPMPLVKGCGDPKWWGAPFTGSSLELGPWSPVSTLEV 346
Qy 317 YSCHPRSPAKRLQLTELQEPALVESDGVKPSFWPMTAQNQSGG SAYSEERDRPYGLVSI 376

Db 347 YSCHPRSPAKRLQLTELQEPALVESDGVKPSFWPMTAQNQSGG SAYSEERDRPYGLVSI 406
Qy 377 DTVTVLDAEGPCTWPCSCEDDGYPALDLDAGLESPGLEDDPLLDAGTTVLSCGCVSAGSP 436
Db 407 DTVTVLDAEGPCTWPCSCEDDGYPALDLDAGLESPGLEDDPLLDAGTTVLSCGCVSAGSP 466
Qy 437 GLGGPLGSLLDRLKPLADGEDWAGGLPWGGRSPGGVSESEAGSPLAGLDMDTFDSGFGV 496
Db 467 GLGGPLGSLLDRLKPLADGEDWAGGLPWGGRSPGGVSESEAGSPLAGLDMDTFDSGFGV 526
Qy 497 SDCSSPVECDFTSPGDEGPPRSYLRQWVIPPPLSSPGPQAS 538
Db 527 SDCSSPVECDFTSPGDEGPPRSYLRQWVIPPPLSSPGPQAS 568

RESULT 11

US-09-404-641-85
; Sequence 85, Application US/09404641
; Patent No. 6576744
; GENERAL INFORMATION:
; APPLICANT: Presnell, Scott R.
; APPLICANT: Conklin, Darrell C.
; APPLICANT: No. 6576744ak, Julia E.
; APPLICANT: Hammond, Angela K.
; TITLE OF INVENTION: CYTOKINE RECEPTOR ZAPLPHALL
; FILE REFERENCE: 98-55
; CURRENT APPLICATION NUMBER: US/09/404,641
; CURRENT FILING DATE: 1999-09-23
; PRIOR FILING DATE: 1999-09-23
; PRIOR APPLICATION NUMBER: US 60/100,896
; PRIOR FILING DATE: 1998-09-23
; PRIOR APPLICATION NUMBER: US 60/123,546
; PRIOR FILING DATE: 1999-03-09
; PRIOR APPLICATION NUMBER: US 60/142,574
; PRIOR FILING DATE: 1999-07-06
; NUMBER OF SEQ ID NOS: 91
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 85
; LENGTH: 529
; TYPE: PRT
; ORGANISM: Mus musculus
US-09-404-641-85

Query Match 58.7%; Score 1735.5; DB 4; Length 529;
Best Local Similarity 62.7%; Pred. No. 1.5e-152;
Matches 340; Conservative 49; Mismatches 136; Indels 17; Gaps 6;
Qy 1 MPRGWAAPLLLLLQGGWCPDLVCYTDYLTQVTCILEMNNLHPSTLTLTWODQYEELKD 60
Db 1 MPRGFWAALLLLILHGAWSCLDLTCYTDYLTWITTCVLETRSPNPSILSLTWODEYEELQD 60
Qy 61 EATSCSLHRSNAHATHATYTCHMDVHFHMADDI FSVNITDQSGNYSCGSLAEISIKP 120
Db 61 QETFCSLHRSNGHTHTIWTCHMRLSQPLSDEVI VNVTDQSGNNSQCGSFVLAESIKP 120
Qy 121 APPENVTVTSGQYNI SWRSYEDPAPFYMKGKQYELQYLRNRPDPAWSPRRKLI SVDS 180
Db 121 APPLNVTVAFSRVDI SWDSAYDEPSNYLGRKQYELQYLRNLRDPVAVRPVTKLISVDS 180
Qy 181 RSVSLLLPLEFRKDSY ELQVRAGMPGSSYOGTWSWSDPVI FQTSBELKEGNPHLL 240
Db 181 RNVSLLEPEFRKDSY YQLQVRAAPQGTSGTSGTWSWSDPVI FQTSBELKEGNPHLL 240
Qy 241 LLLLVIVIFAPFWSLKTHTPLWRLWKKIWA-VPSPERFPMPLVKGCGDPKWWGAPFTGS 299
Db 241 LLAVLIIVL-VFMGLKHLPHRLWKKIWA PVTPTESFQPLYREHSGNFKKWVNTPTTAS 299
Qy 300 SLELGPWSPVSTLEV YSCHPRSPAKRLQLTELQEPALVESDGVKPSFW---PTAQ 356
Db 300 SIELVQSSSTTSAL-----HLSLYPAKEKFPGLGLEQLECDGMSGPHGWCIIPLAA 354
Qy 357 NSGGSAYSEERDRPYGLVSI DTVTVLDAEGPCTWPCSCEDDGYPALDLDAGLESPGLEDD 416
Db 355 QGAVSAYSEERDRPYGLVSI DTVTVGDAEGLCVWPCSCEDDGYPAMNLDAGREGPNSED 414

QY 417 PLLDAGTTVLSCGVSAGSPGLGGPLGSLDLRLKPLADGEDWAGGLPMGGRSPGGSVS 476
Db 415 LLLVTDPAFLSCGVSAGSGLRGLGSPGSLDLRLSLFAKEGDTWADPTWRTGSPGGSVS 474
QY 477 EAGSPLAGLMDTDFDSGFGVSGDCSSPVECDFTSPGDEGPPRSYLROWVVIPLPLSSPGQ 536
Db 475 EAGSP-PGLMDTDFDSGFGAGSCGSPVET-----DEGPPRSYLROWVVRTPPVDSGAQ 527
QY 537 AS 538
Db 528 SS 529

RESULT 12

US-10-414-186-85
; Sequence 85, Application US/10414186
; Patent No. 6692924

GENERAL INFORMATION:

; APPLICANT: Presnell, Scott R.
; APPLICANT: Conklin, Darrell C.
; APPLICANT: No. 6692924k, Julia E.
; APPLICANT: Hammond, Angela K.
; TITLE OF INVENTION: CYTOKINE RECEPTOR ZAPLHALL
; FILE REFERENCE: 98-55
; CURRENT APPLICATION NUMBER: US/10/414,186
; PRIOR FILING DATE: 2003-04-14
; PRIOR APPLICATION NUMBER: US/09/404,641
; PRIOR FILING DATE: 1999-09-23
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: US 60/100,896
; PRIOR FILING DATE: EARLIER FILING DATE: 1998-09-23
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: US 60/123,546
; PRIOR FILING DATE: EARLIER FILING DATE: 1999-03-09
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: US 60/142,574
; PRIOR FILING DATE: EARLIER FILING DATE: 1999-07-06
; NUMBER OF SEQ ID NOS: 91
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 85
; LENGTH: 529
; TYPE: PRT
; ORGANISM: Mus musculus

US-10-414-186-85

Query Match 58.7%; Score 1735.5; DB 4; Length 529;

Best Local Similarity 62.7%; Pred. No. 1.5e-152;

Matches 340; Conservative 49; Mismatches 136; Indels 17; Gaps 6;

QY 1 MPRGWAAPLILLLLOGGCGPDLVCYTDYLOTVICILEMNLHPSTLTLTWDOYEELKD 60
Db 1 MPRGVAALLLILHGAWSCLDLTCYTDYLTITCVLETRSPNPSILSLTWODEYEELQD 60
QY 61 EATCSLHRSAHNATHATYTCMDVHFHMADDIFSVNITDQSGNYSQEGCSFLLAESIKP 120
Db 61 QETFCSLHRSAGHNTTHIWTCHMRSLQFLSDEVFVNVTDQSGNNSQEGCSFVLAESIKP 120
QY 121 APPFNVTTFSGQYNISWRSDYEDPAFMYLKGKLOLQYELQYRNRPDPAVPRKLIISVDS 180
Db 121 APPLNVTVAFGSDYDISWDSAYDEPSNYVLRGKLOLQYELQYRNLRDPYAVRPVTKLIISVDS 180
QY 181 RSVSLPLLEFRKDSYELQVRAAGPMGSSYQGTWSESDPVIPTQSEELKEGWNPHLL 240
Db 181 RNVSLLPEEFKDSYQLOVRAAPQGTSGFRGTWSESDPVIPTQAGEPEAGNDPHMLL 240
QY 241 LLLLVIVTFAPWSLTKTHPLRLWKIWA-VPSPERFFMPLYKGCSDGPKKVVGAPFTGS 299
Db 241 LLAVLIIVL-VFMGLKIHLPLRLWKIWAIVPTPESFPQPLYREHSGNFKKWNVTPTAS 299
QY 300 SLELGPWSEVPSTLEVYSCHPRPAPKRLQLOTELQEPALVESDGVKPKPSFW---PTAQ 356
Db 300 SIELVQSSSTTTTSA-----HLSLYPAKEKPPGLGLEEQLECDGMESEPGHWCIIPLAA 354
QY 357 NSGGSAYSEERDRPYGLVSIIDTVTLDAGGCTWPCSCDDGYPALDLDAGLEPSPGLE 416

Db 355 GOAVSAYSEERDRPYGLVSIIDTVTVDAGELCWPCSCDDGYPAMNLDAGRESGPNSED 414
QY 417 PLLDAGTTVLSCGVSAGSPGLGGPLGSLDLRLKPLADGEDWAGGLPMGGRSPGGSVS 476
Db 415 LLLVTDPAFLSCGVSAGSGLRGLGSPGSLDLRLSLFAKEGDTWADPTWRTGSPGGSVS 474
QY 477 EAGSPLAGLMDTDFDSGFGVSGDCSSPVECDFTSPGDEGPPRSYLROWVVIPLPLSSPGQ 536
Db 475 EAGSP-PGLMDTDFDSGFGAGSCGSPVET-----DEGPPRSYLROWVVRTPPVDSGAQ 527
QY 537 AS 538
Db 528 SS 529

RESULT 13

US-09-825-561A-12

; Sequence 12, Application US/09825561A

; Patent No. 6777539

GENERAL INFORMATION:

; APPLICANT: Sprecher, Cindy A.
; APPLICANT: No. 6777539ak, Julia E.
; APPLICANT: West, James W.
; APPLICANT: Presnell, Scott R.
; APPLICANT: Holly, Richard D.
; APPLICANT: Nelson, Andrew J.
; TITLE OF INVENTION: SOLUBLE ZAPLHALL CYTOKINE RECEPTORS
; FILE REFERENCE: 00-22
; CURRENT APPLICATION NUMBER: US/09/825,561A
; CURRENT FILING DATE: 2000-04-05
; PRIOR APPLICATION NUMBER: US 60/194,731
; PRIOR FILING DATE: 2000-04-05
; PRIOR APPLICATION NUMBER: US 60/222,121
; PRIOR FILING DATE: 2000-07-28
; NUMBER OF SEQ ID NOS: 86
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 12
; LENGTH: 529
; TYPE: PRT
; ORGANISM: mus musculus

US-09-825-561A-12

Query Match 58.7%; Score 1735.5; DB 4; Length 529;

Best Local Similarity 62.7%; Pred. No. 1.5e-152;

Matches 340; Conservative 49; Mismatches 136; Indels 17; Gaps 6;

QY 1 MPRGWAAPLILLLLOGGCGPDLVCYTDYLOTVICILEMNLHPSTLTLTWDOYEELKD 60
Db 1 MPRGVAALLLILHGAWSCLDLTCYTDYLTITCVLETRSPNPSILSLTWODEYEELQD 60
QY 61 EATCSLHRSAHNATHATYTCMDVHFHMADDIFSVNITDQSGNYSQEGCSFLLAESIKP 120
Db 61 QETFCSLHRSAGHNTTHIWTCHMRSLQFLSDEVFVNVTDQSGNNSQEGCSFVLAESIKP 120
QY 121 APPFNVTTFSGQYNISWRSDYEDPAFMYLKGKLOLQYELQYRNRPDPAVPRKLIISVDS 180
Db 121 APPLNVTVAFGSDYDISWDSAYDEPSNYVLRGKLOLQYELQYRNLRDPYAVRPVTKLIISVDS 180
QY 181 RSVSLPLLEFRKDSYELQVRAAGPMGSSYQGTWSESDPVIPTQSEELKEGWNPHLL 240
Db 181 RNVSLLPEEFKDSYQLOVRAAPQGTSGFRGTWSESDPVIPTQAGEPEAGNDPHMLL 240
QY 241 LLLLVIVTFAPWSLTKTHPLRLWKIWA-VPSPERFFMPLYKGCSDGPKKVVGAPFTGS 299
Db 241 LLAVLIIVL-VFMGLKIHLPLRLWKIWAIVPTPESFPQPLYREHSGNFKKWNVTPTAS 299
QY 300 SLELGPWSEVPSTLEVYSCHPRPAPKRLQLOTELQEPALVESDGVKPKPSFW---PTAQ 356
Db 300 SIELVQSSSTTTTSA-----HLSLYPAKEKPPGLGLEEQLECDGMESEPGHWCIIPLAA 354
QY 357 NSGGSAYSEERDRPYGLVSIIDTVTLDAGGCTWPCSCDDGYPALDLDAGLEPSPGLE 416
Db 355 GOAVSAYSEERDRPYGLVSIIDTVTVDAGELCWPCSCDDGYPAMNLDAGRESGPNSED 414

Qy 417 PLLDAGTTLVSCGCVSAGSPGLGGPLGSLDLRLKPLADGEDWAGGLPWGGRSPGGVSES 476
Db 415 LLLVTDPAFLSCGCVSGSLRGLGSPGSLDLRLKLSFAKEGDWTADPTWRTGSPGGSES 474
Qy 477 EAGSPAGLMDTDFDSGVGSDCSPVBCDFTSPGDEGPPRSYLRQWVVIPIPLSSPPQ 536
Db 475 EAGSP-PGLDMDTDFDSGAGSDGSPVET-----DEGPPRSYLRQWVVRTPPPVDSGAQ 527
Qy 537 AS 538
Db 528 SS 529
RESULT 14
US-10-243-072-85
; Sequence 85, Application US/10243072
; Patent No. 6803451
; GENERAL INFORMATION:
; APPLICANT: Presnelli, Scott R.
; APPLICANT: Conklin, Darrrell C.
; APPLICANT: No. 6803451ak, Julia E.
; APPLICANT: Hammond, Angela K.
; TITLE OF INVENTION: CYTOKINE RECEPTOR ZAPLHALL
; FILE REFERENCE: 98-55C1
; CURRENT APPLICATION NUMBER: US/10/243,072
; CURRENT FILING DATE: 2002-09-13
; PRIOR APPLICATION NUMBER: 09/628,127
; PRIOR FILING DATE: 2000-07-28
; PRIOR APPLICATION NUMBER: US 60/100,896
; PRIOR FILING DATE: 1998-09-23
; PRIOR APPLICATION NUMBER: US 60/123,546
; PRIOR FILING DATE: 1999-03-09
; PRIOR APPLICATION NUMBER: US 60/142,574
; PRIOR FILING DATE: 1999-07-06
; PRIOR APPLICATION NUMBER: US 09/404,641
; PRIOR FILING DATE: 1999-09-23
; NUMBER OF SEQ ID NOS: 92
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 85
; LENGTH: 529
; TYPE: PRT
; ORGANISM: Mus musculus
US-10-243-072-85

Query Match 58.7%; Score 1735.5; DB 4; Length 529;
Best Local Similarity 62.7%; Pred. No. 1.5e-152;
Matches 340; Conservative 49; Mismatches 136; Indels 17; Gaps 6;
Qy 1 MPRGWAAPLLLLLOGGWCPCDLVCTDYLTQVICILEMNLHPSTLTWQDOYEELKD 60
Db 1 MPRGVAALLLLILHGAWSCLDLCTCYTDYLTITCVLETRSPNPSILSLTWQDEYEELQD 60
Qy 61 EATSCSLHRSNAHNAHATHTTCHMDVFFHMADDIFSVNITDQSGNYSQCGSFLLAESIKP 120
Db 61 QETFCSLHRSNGHNTHTTCHMRLSQFLSDEVFVNVITDQSGNNSQCGSFVLAESIKP 120
Qy 121 APPFNVTTFSGQYNISWRSDYEDPAFYMKGKLOEYLOQYRNRPDPWAVSPRRKLISVDS 180
Db 121 APPLNVTVAFSGRYDISWDSAYDEPSNYVLRGKLOEYLOQYRNLRDPYAVRPVTKLISVDS 180
Qy 181 RSVSLPLLEFRKDSYELQVRAGMPGSSYOGTWSWSDPVIPTQSEELKEGNPHLL 240
Db 61 QETFCSLHRSNGHNTHTTCHMRLSQFLSDEVFVNVITDQSGNNSQCGSFVLAESIKP 120
Qy 121 APPFNVTTFSGQYNISWRSDYEDPAFYMKGKLOEYLOQYRNRPDPWAVSPRRKLISVDS 180
Db 121 APPLNVTVAFSGRYDISWDSAYDEPSNYVLRGKLOEYLOQYRNLRDPYAVRPVTKLISVDS 180
Qy 181 RSVSLPLLEFRKDSYELQVRAGMPGSSYOGTWSWSDPVIPTQSEELKEGNPHLL 240
Db 181 RNVSLPLLEFRKDSYELQVRAGMPGSSYOGTWSWSDPVIPTQSEELKEGNPHLL 240
Qy 241 LLLVIVIPAFWSLTKHPLRLWKIWA-VPSPERFFMPLYKCGDFKKWVGPFTGS 299
Db 241 LLLVIVIPAFWSLTKHPLRLWKIWA-VPSPERFFMPLYKCGDFKKWVGPFTGS 299
Qy 300 SLELGPWSPVSTLEVVSCHPPRPSPAKRLQLTELQEPALVESDGVKPSFW---PTAQ 356
Db 300 SLELGPWSPVSTLEVVSCHPPRPSPAKRLQLTELQEPALVESDGVKPSFW---PTAQ 356
Qy 241 LLLVIVIPAFWSLTKHPLRLWKIWA-VPSPERFFMPLYKCGDFKKWVGPFTGS 299
Db 241 LLLVIVIPAFWSLTKHPLRLWKIWA-VPSPERFFMPLYKCGDFKKWVGPFTGS 299
Qy 300 SLELGPWSPVSTLEVVSCHPPRPSPAKRLQLTELQEPALVESDGVKPSFW---PTAQ 356
Db 300 SLELGPWSPVSTLEVVSCHPPRPSPAKRLQLTELQEPALVESDGVKPSFW---PTAQ 356

Qy 357 NSGGSAYSEERDRPYGLVSDITVTVLDAEGCTWPCSCDDGYPALDLADGLESPGLE 416
Db 355 GOAVSAYSEERDRPYGLVSDITVTVGDAEGLCWPCSCDDGYPAMNLDAGRESGPNSD 414
Qy 417 PLLDAGTTLVSCGCVSAGSPGLGGPLGSLDLRLKPLADGEDWAGGLPWGGRSPGGVSES 476
Db 415 LLLVTDPAFLSCGCVSGSLRGLGSPGSLDLRLKLSFAKEGDWTADPTWRTGSPGGSES 474
Qy 477 EAGSPAGLMDTDFDSGVGSDCSPVBCDFTSPGDEGPPRSYLRQWVVIPIPLSSPPQ 536
Db 475 EAGSP-PGLDMDTDFDSGAGSDGSPVET-----DEGPPRSYLRQWVVRTPPPVDSGAQ 527
Qy 537 AS 538
Db 528 SS 529
RESULT 15
US-09-732-234-6
; Sequence 6, Application US/09732234
; Patent No. 6586251
; GENERAL INFORMATION:
; APPLICANT: Murphy, et al.
; TITLE OF INVENTION: METHODS OF MODIFYING EUKARYOTIC CELLS
; FILE REFERENCE: REG 780A
; CURRENT APPLICATION NUMBER: US/09/732,234
; CURRENT FILING DATE: 2000-12-07
; NUMBER OF SEQ ID NOS: 6
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 6
; LENGTH: 529
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Mouse OCR10 protein
US-09-732-234-6

Query Match 58.5%; Score 1729.5; DB 4; Length 529;
Best Local Similarity 62.4%; Pred. No. 5.4e-152;
Matches 338; Conservative 51; Mismatches 136; Indels 17; Gaps 6;
Qy 1 MPRGWAAPLLLLLOGGWCPCDLVCTDYLTQVICILEMNLHPSTLTWQDOYEELKD 60
Db 1 MPRGVAALLLLILHGAWSCLDLCTCYTDYLTITCVLETRSPNPSILSLTWQDEYEELQD 60
Qy 61 EATSCSLHRSNAHNAHATHTTCHMDVFFHMADDIFSVNITDQSGNYSQCGSFLLAESIKP 120
Db 61 QETFCSLHRSNGHNTHTTCHMRLSQFLSDEVFVNVITDQSGNNSQCGSFVLAESIKP 120
Qy 121 APPFNVTTFSGQYNISWRSDYEDPAFYMKGKLOEYLOQYRNRPDPWAVSPRRKLISVDS 180
Db 121 APPLNVTVAFSGRYDISWDSAYDEPSNYVLRGKLOEYLOQYRNLRDPYAVRPVTKLISVDS 180
Qy 181 RSVSLPLLEFRKDSYELQVRAGMPGSSYOGTWSWSDPVIPTQSEELKEGNPHLL 240
Db 181 RNVSLPLLEFRKDSYELQVRAGMPGSSYOGTWSWSDPVIPTQSEELKEGNPHLL 240
Qy 241 LLLVIVIPAFWSLTKHPLRLWKIWA-VPSPERFFMPLYKCGDFKKWVGPFTGS 299
Db 241 LLLVIVIPAFWSLTKHPLRLWKIWA-VPSPERFFMPLYKCGDFKKWVGPFTGS 299
Qy 300 SLELGPWSPVSTLEVVSCHPPRPSPAKRLQLTELQEPALVESDGVKPSFW---PTAQ 356
Db 300 SLELGPWSPVSTLEVVSCHPPRPSPAKRLQLTELQEPALVESDGVKPSFW---PTAQ 356
Qy 357 NSGGSAYSEERDRPYGLVSDITVTVLDAEGCTWPCSCDDGYPALDLADGLESPGLE 416
Db 355 GOAVSAYSEERDRPYGLVSDITVTVGDAEGLCWPCSCDDGYPAMNLDAGRESGPNSD 414
Qy 417 PLLDAGTTLVSCGCVSAGSPGLGGPLGSLDLRLKPLADGEDWAGGLPWGGRSPGGVSES 476
Db 415 LLLVTDPAFLSCGCVSGSLRGLGSPGSLDLRLKLSFAKEGDWTADPTWRTGSPGGSES 474

Qy	477	EAGSPLAGLDMDTFDSDGFGVSDCSPVCECDFTSPGDEGPPRSYLROWVVI	PPPLSSPCPQ	536
Db	475	EAGSP-PGLDMDTFDSDGFGVSDCSPVCECDFTSPGDEGPPRSYLROWVVI	PPPLSSPCPQ	527
Qy	537	AS	538	
Db	528	SS	529	

Search completed: July 9, 2005, 11:48:39
Job time : 44 secs

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GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: July 9, 2005, 11:44:05 ; Search time 65 Seconds
(without alignments)
1080.022 Million cell updates/sec

Title: US-10-620-169-4

Perfect score: 2958

Sequence: 1 MPRGWAAPLLLLLLQGWGC.....YLRQWVPPPLSSFGPQAS 538

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 614041 seqs, 130485892 residues

Total number of hits satisfying chosen parameters: 614041

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

- Pending Patents AA New.*
- 1: /cgn2_6/prodata/2/paa/PCT_NEW_COMB.pep.*
 - 2: /cgn2_6/prodata/2/paa/US06_NEW_COMB.pep.*
 - 3: /cgn2_6/prodata/2/paa/US07_NEW_COMB.pep.*
 - 4: /cgn2_6/prodata/2/paa/US08_NEW_COMB.pep.*
 - 5: /cgn2_6/prodata/2/paa/US09_NEW_COMB.pep.*
 - 6: /cgn2_6/prodata/2/paa/US10_NEW_COMB.pep.*
 - 7: /cgn2_6/prodata/2/paa/US11_NEW_COMB.pep.*
 - 8: /cgn2_6/prodata/2/paa/US60_NEW_COMB.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	2958	100.0	538	1	PCT-US03-28361-82
2	2958	100.0	538	1	PCT-US05-17514-6
3	2958	100.0	538	7	US-11-132-947-6
4	2958	100.0	547	6	US-10-940-774A-11544
5	1735.5	58.7	529	1	PCT-US05-17514-8
6	1735.5	58.7	529	7	US-11-132-947-8
7	1302	44.0	384	1	PCT-US05-07590-32
8	1302	44.0	384	7	US-11-075-351-32
9	278	9.4	551	1	PCT-US03-10870-439
10	278	9.4	551	7	US-11-033-545-308
11	278	9.4	551	8	US-60-685-372-1266
12	278	9.4	594	7	US-11-033-545-537
13	256	8.7	525	7	US-11-021-951-151
14	231	7.8	536	6	US-10-940-774A-6185
15	219.5	7.4	823	1	PCT-US04-17028-11
16	216	7.3	508	5	US-09-016-159D-7
17	215.5	7.3	521	1	PCT-US05-12464-58
18	215.5	7.3	521	7	US-11-105-268-58
19	215	7.3	522	6	US-10-412-703B-126
20	215	7.3	522	6	US-10-940-774A-6185
21	214	7.2	533	6	US-10-940-774A-9753
22	213	7.2	508	5	US-09-016-159D-5
23	211.5	7.2	896	1	PCT-US04-42360-2373
24	206	7.0	897	1	PCT-US05-15207-2184
25	206	7.0	897	8	US-60-685-372-1262

26	202.5	6.8	818	1	PCT-US04-17028-10	Sequence 10, Appl
27	193.5	6.5	825	1	PCT-US05-02350-130	Sequence 130, Appl
28	193.5	6.5	825	1	PCT-US04-17028-14	Sequence 14, Appl
29	193.5	6.5	825	6	US-10-287-436A-385	Sequence 385, Appl
30	193.5	6.5	825	6	US-10-287-436A-390	Sequence 390, Appl
31	193.5	6.5	825	6	US-10-287-436A-1085	Sequence 1085, Appl
32	193.5	6.5	825	6	US-10-287-436A-1090	Sequence 1090, Appl
33	193.5	6.5	825	7	US-11-043-770-130	Sequence 130, Appl
34	177	6.0	379	7	US-11-052-527-8	Sequence 8, Appl
35	177	6.0	379	7	US-11-052-527-8	Sequence 8, Appl
36	176	5.9	371	7	US-11-052-527-5	Sequence 5, Appl
37	176	5.9	371	7	US-11-052-527-5	Sequence 5, Appl
38	170	5.7	809	1	PCT-US04-17028-2	Sequence 2, Appl
39	170	5.7	809	1	PCT-US04-17028-15	Sequence 15, Appl
40	168.5	5.7	635	1	PCT-US05-15207-1589	Sequence 1589, Appl
41	168	5.7	369	7	US-11-052-527-12	Sequence 12, Appl
42	168	5.7	369	7	US-11-052-527-12	Sequence 12, Appl
43	162.5	5.5	223	1	PCT-US04-17028-9	Sequence 9, Appl
44	162.5	5.5	223	1	PCT-US04-17028-18	Sequence 18, Appl
45	162.5	5.5	357	7	US-11-052-527-9	Sequence 9, Appl

ALIGNMENTS

RESULT 1

PCT-US03-28361-82

; Sequence 82, Application PC/TUS0328361

; GENERAL INFORMATION:

; APPLICANT: GENENTECH, INC.

; APPLICANT: SARAH C. BODARY

; APPLICANT: HILARY CLARK

; APPLICANT: BRISDELL HUNTE

; APPLICANT: JANET K. JACKMAN

; APPLICANT: JILL SCHOENFELD

; APPLICANT: P. MICKEY WILLIAMS

; APPLICANT: WILLIAM I. WOOD

; APPLICANT: THOMAS D. WU

; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE TREATMENT OF IMMUNE

; FILE REFERENCE: P1975R1-PCT

; CURRENT APPLICATION NUMBER: PCT/US03/28361

; CURRENT FILING DATE: 2003-09-10

; PRIOR APPLICATION NUMBER: US 60/410,174

; PRIOR FILING DATE: 2002-09-11

; NUMBER OF SEQ ID NOS: 104

; SEQ ID NO 82

; LENGTH: 538

; TYPE: PRT

; ORGANISM: Homo sapiens

PCT-US03-28361-82

Query Match 100.0%; Score 2958; DB 1; Length 538;
Best Local Similarity 100.0%; Pred. No. 4.1e-201; Indels 0; Gaps 0;
Matches 538; Conservative 0; Mismatches 0;

QY	1	MPRGWAAPLLLLLLQGWGCPDVCYDYLTQTVICILEMNLHPSTLTITWQDQYEELKD	60
Db	1	MPRGWAAPLLLLLLQGWGCPDVCYDYLTQTVICILEMNLHPSTLTITWQDQYEELKD	60
QY	61	EATSCSLHRSAHNATHATYTCMDVHFHMADDFSVNITDQSGNYSQECGSPFLAESIKP	120
Db	61	EATSCSLHRSAHNATHATYTCMDVHFHMADDFSVNITDQSGNYSQECGSPFLAESIKP	120
QY	121	APPFNVTTFSGOYNISMRSDYEDPAFYMLKGLQYELQYRNRGDPWAVSPRKLISVDS	180
Db	121	APPFNVTTFSGOYNISMRSDYEDPAFYMLKGLQYELQYRNRGDPWAVSPRKLISVDS	180
QY	181	RSVSLPLLEFRKDSSEYELQVRAGMPGSSYQGTWSESDPVIPTQSEELKEGWNPHLLL	240
Db	181	RSVSLPLLEFRKDSSEYELQVRAGMPGSSYQGTWSESDPVIPTQSEELKEGWNPHLLL	240
QY	241	LLLLLVIFAPFWSLTKTHPLWRLWKKIWAVSPERFFMPLYKGCSDGDFKWWGAPFTGSS	300

Db 241 LLLLIVIFAPFWSLKTPLWRLWKIWAIVSPERFMPPLYKGCSDGFKKWGAPFTGSS 300
QY 301 LELGWSPEVSTLEVYCHPPSPAKRLQLTLOEPAELVESDGVKPKSPFWPTAQNSSG 360
Db 301 LELGWSPEVSTLEVYCHPPSPAKRLQLTLOEPAELVESDGVKPKSPFWPTAQNSSG 360
QY 361 SAYSEERDRPYGLVSIIDTVTLDAEGPCTWPCSCDDGYPALDDAGLESPGLEDPILLD 420
Db 361 SAYSEERDRPYGLVSIIDTVTLDAEGPCTWPCSCDDGYPALDDAGLESPGLEDPILLD 420
QY 421 AGTTVLSCGCVSAGSPGLGGPLGSLDLRLKPLADGEDWAGGLPWGGRSPGCVSESEAGS 480
Db 421 AGTTVLSCGCVSAGSPGLGGPLGSLDLRLKPLADGEDWAGGLPWGGRSPGCVSESEAGS 480
QY 481 PLAGLDMDTFDSGFGVSDCSPVECDFTSPGDEGPPRSYLRQWVVIPLPSSPGPQAS 538
Db 481 PLAGLDMDTFDSGFGVSDCSPVECDFTSPGDEGPPRSYLRQWVVIPLPSSPGPQAS 538
RESULT 2
PCT-US05-17514-6
; Sequence 6, Application PC/TUS0517514
; GENERAL INFORMATION:
; APPLICANT: Wyeth
; APPLICANT: Kasaian, Marion
; APPLICANT: Wood, Nancy L.
; APPLICANT: Donaldson, Debra D.
; APPLICANT: Collins, Mary
; TITLE OF INVENTION: MODULATION OF IMMUNOGLOBULIN PRODUCTION AND ATOPIC DISORDERS
; FILE REFERENCE: 16158-016W01
; CURRENT FILING DATE: 2005-05-24
; PRIOR APPLICATION NUMBER: US 60/572,407
; PRIOR FILING DATE: 2004-05-19
; NUMBER OF SEQ ID NOS: 12
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 6
; LENGTH: 538
; TYPE: PRT
; ORGANISM: Homo sapiens
PCT-US05-17514-6
Query Match 100.0%; Score 2958; DB 1; Length 538;
Best Local Similarity 100.0%; Pred. No. 4.1e-201;
Matches 538; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 MPRGWAAPLLLLLQGGWGPCDLVCYTDYLTQTVICILEMMNLHPSTLTLTWQDQYEELKD 60
Db 1 MPRGWAAPLLLLLQGGWGPCDLVCYTDYLTQTVICILEMMNLHPSTLTLTWQDQYEELKD 60
QY 61 EATCSLHRSAHNATHATYTCMDVHFHMADDIFSUNITDQSGNYSQBCGFLLAESIKP 120
Db 61 EATCSLHRSAHNATHATYTCMDVHFHMADDIFSUNITDQSGNYSQBCGFLLAESIKP 120
QY 121 APPENVVTFSGQYNIWSRSDYEDPAFYMLKGKQYLOEYLRNRPDPAVSPRRKLIISVDS 180
Db 121 APPENVVTFSGQYNIWSRSDYEDPAFYMLKGKQYLOEYLRNRPDPAVSPRRKLIISVDS 180
QY 181 RSVSLLPLEFRKDSSEYELQVRAGMPGSSYQGTWSESDPVI FQTQSEELKEGWNPHLLL 240
Db 181 RSVSLLPLEFRKDSSEYELQVRAGMPGSSYQGTWSESDPVI FQTQSEELKEGWNPHLLL 240
QY 241 LLLLIVIFAPFWSLKTPLWRLWKIWAIVSPERFMPPLYKGCSDGFKKWGAPFTGSS 300
Db 241 LLLLIVIFAPFWSLKTPLWRLWKIWAIVSPERFMPPLYKGCSDGFKKWGAPFTGSS 300
QY 301 LELGWSPEVSTLEVYCHPPSPAKRLQLTLOEPAELVESDGVKPKSPFWPTAQNSSG 360
Db 301 LELGWSPEVSTLEVYCHPPSPAKRLQLTLOEPAELVESDGVKPKSPFWPTAQNSSG 360
QY 361 SAYSEERDRPYGLVSIIDTVTLDAEGPCTWPCSCDDGYPALDDAGLESPGLEDPILLD 420
Db 361 SAYSEERDRPYGLVSIIDTVTLDAEGPCTWPCSCDDGYPALDDAGLESPGLEDPILLD 420
QY 421 AGTTVLSCGCVSAGSPGLGGPLGSLDLRLKPLADGEDWAGGLPWGGRSPGCVSESEAGS 480
Db 421 AGTTVLSCGCVSAGSPGLGGPLGSLDLRLKPLADGEDWAGGLPWGGRSPGCVSESEAGS 480
QY 481 PLAGLDMDTFDSGFGVSDCSPVECDFTSPGDEGPPRSYLRQWVVIPLPSSPGPQAS 538
Db 481 PLAGLDMDTFDSGFGVSDCSPVECDFTSPGDEGPPRSYLRQWVVIPLPSSPGPQAS 538

Db 361 SAYSEERDRPYGLVSIIDTVTLDAEGPCTWPCSCDDGYPALDDAGLESPGLEDPILLD 420
QY 421 AGTTVLSCGCVSAGSPGLGGPLGSLDLRLKPLADGEDWAGGLPWGGRSPGCVSESEAGS 480
Db 421 AGTTVLSCGCVSAGSPGLGGPLGSLDLRLKPLADGEDWAGGLPWGGRSPGCVSESEAGS 480
QY 481 PLAGLDMDTFDSGFGVSDCSPVECDFTSPGDEGPPRSYLRQWVVIPLPSSPGPQAS 538
Db 481 PLAGLDMDTFDSGFGVSDCSPVECDFTSPGDEGPPRSYLRQWVVIPLPSSPGPQAS 538
RESULT 3
US-11-132-947-6
; Sequence 6, Application US/11132947
; GENERAL INFORMATION:
; APPLICANT: Kasaian, Marion
; APPLICANT: Wood, Nancy L.
; APPLICANT: Donaldson, Debra D.
; APPLICANT: Collins, Mary
; TITLE OF INVENTION: MODULATION OF IMMUNOGLOBULIN PRODUCTION AND ATOPIC DISORDERS
; FILE REFERENCE: 16158-016001
; CURRENT APPLICATION NUMBER: US/11/132,947
; CURRENT FILING DATE: 2005-05-19
; PRIOR APPLICATION NUMBER: US 60/572,407
; PRIOR FILING DATE: 2004-05-19
; NUMBER OF SEQ ID NOS: 12
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 6
; LENGTH: 538
; TYPE: PRT
; ORGANISM: Homo sapiens
US-11-132-947-6
Query Match 100.0%; Score 2958; DB 7; Length 538;
Best Local Similarity 100.0%; Pred. No. 4.1e-201;
Matches 538; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 MPRGWAAPLLLLLQGGWGPCDLVCYTDYLTQTVICILEMMNLHPSTLTLTWQDQYEELKD 60
Db 1 MPRGWAAPLLLLLQGGWGPCDLVCYTDYLTQTVICILEMMNLHPSTLTLTWQDQYEELKD 60
QY 61 EATCSLHRSAHNATHATYTCMDVHFHMADDIFSUNITDQSGNYSQBCGFLLAESIKP 120
Db 61 EATCSLHRSAHNATHATYTCMDVHFHMADDIFSUNITDQSGNYSQBCGFLLAESIKP 120
QY 121 APPENVVTFSGQYNIWSRSDYEDPAFYMLKGKQYLOEYLRNRPDPAVSPRRKLIISVDS 180
Db 121 APPENVVTFSGQYNIWSRSDYEDPAFYMLKGKQYLOEYLRNRPDPAVSPRRKLIISVDS 180
QY 181 RSVSLLPLEFRKDSSEYELQVRAGMPGSSYQGTWSESDPVI FQTQSEELKEGWNPHLLL 240
Db 181 RSVSLLPLEFRKDSSEYELQVRAGMPGSSYQGTWSESDPVI FQTQSEELKEGWNPHLLL 240
QY 241 LLLLIVIFAPFWSLKTPLWRLWKIWAIVSPERFMPPLYKGCSDGFKKWGAPFTGSS 300
Db 241 LLLLIVIFAPFWSLKTPLWRLWKIWAIVSPERFMPPLYKGCSDGFKKWGAPFTGSS 300
QY 301 LELGWSPEVSTLEVYCHPPSPAKRLQLTLOEPAELVESDGVKPKSPFWPTAQNSSG 360
Db 301 LELGWSPEVSTLEVYCHPPSPAKRLQLTLOEPAELVESDGVKPKSPFWPTAQNSSG 360
QY 361 SAYSEERDRPYGLVSIIDTVTLDAEGPCTWPCSCDDGYPALDDAGLESPGLEDPILLD 420
Db 361 SAYSEERDRPYGLVSIIDTVTLDAEGPCTWPCSCDDGYPALDDAGLESPGLEDPILLD 420
QY 421 AGTTVLSCGCVSAGSPGLGGPLGSLDLRLKPLADGEDWAGGLPWGGRSPGCVSESEAGS 480
Db 421 AGTTVLSCGCVSAGSPGLGGPLGSLDLRLKPLADGEDWAGGLPWGGRSPGCVSESEAGS 480
QY 481 PLAGLDMDTFDSGFGVSDCSPVECDFTSPGDEGPPRSYLRQWVVIPLPSSPGPQAS 538
Db 481 PLAGLDMDTFDSGFGVSDCSPVECDFTSPGDEGPPRSYLRQWVVIPLPSSPGPQAS 538

RESULT 4

US-10-940-774A-11544
; Sequence 11544, Application US/10940774A
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CLO01307
; CURRENT APPLICATION NUMBER: US/10/940,774A
; CURRENT FILING DATE: 2004-09-15
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 11544
; LENGTH: 547
; TYPE: PRT
; ORGANISM: Human
US-10-940-774A-11544

Query Match 100.0%; Score 2958; DB 6; Length 547;
Best Local Similarity 100.0%; Pred. No. 4.2e-201;
Matches 538; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MPRGWAAPLLLLLQGGGCPDLVCYTDYQVVICILEMNNLHPSTLTLTWQDQVEELKD 60
DB 10 MPRGWAAPLLLLLQGGGCPDLVCYTDYQVVICILEMNNLHPSTLTLTWQDQVEELKD 69

QY 61 EATCSLHRSAHNATHATYTCMDVHFHMADDIFSVNITDQSGNYSQBCSFLLAESIKP 120
DB 70 EATCSLHRSAHNATHATYTCMDVHFHMADDIFSVNITDQSGNYSQBCSFLLAESIKP 129

QY 121 APPFNVTTFSGQYNISWRSDYEDPAFYMLKGKQYELQYRNRPDPWAVSPRRKLIISVDS 180
DB 130 APPFNVTTFSGQYNISWRSDYEDPAFYMLKGKQYELQYRNRPDPWAVSPRRKLIISVDS 189

QY 181 RSVLLPLEFRKDSYELQVRAGPMGSSYQGTWSEWSDPVI FQTSBELKEGWNPHLL 240
DB 190 RSVLLPLEFRKDSYELQVRAGPMGSSYQGTWSEWSDPVI FQTSBELKEGWNPHLL 249

QY 241 LLLLIVVIFAPFWSLTKTHPLWRLMKKIWA VPSPERFMPLYKGCSDGFKWVGAPFTGSS 300
DB 250 LLLLIVVIFAPFWSLTKTHPLWRLMKKIWA VPSPERFMPLYKGCSDGFKWVGAPFTGSS 309

QY 301 LELGWSPEVPTLEVYSCHPSPSPAKRLQLTLEQPAELVESDGVKPSFVWPTAQN 360
DB 310 LELGWSPEVPTLEVYSCHPSPSPAKRLQLTLEQPAELVESDGVKPSFVWPTAQN 369

QY 361 SAYSEERDRPYGLVSDITVTVLDAEGCTWPCSCDDGYPALDLDAGLEPSGLDPLD 420
DB 370 SAYSEERDRPYGLVSDITVTVLDAEGCTWPCSCDDGYPALDLDAGLEPSGLDPLD 429

QY 421 AGTTVLSCGVSAGSFGGLGSLDLRLKPLPADGEDWAGGLPWGGRSPGCVSEAGS 480
DB 430 AGTTVLSCGVSAGSFGGLGSLDLRLKPLPADGEDWAGGLPWGGRSPGCVSEAGS 489

QY 481 PLAGLMDTDFSGFVSGSDCSSPVECDFTSPGDEGPPRSYLRQWVIPPPLSSPGQAS 538
DB 490 PLAGLMDTDFSGFVSGSDCSSPVECDFTSPGDEGPPRSYLRQWVIPPPLSSPGQAS 547

RESULT 5

PCT-US05-17514-8
; Sequence 8, Application PC/TUS0517514
; GENERAL INFORMATION:
; APPLICANT: Wyeth
; APPLICANT: Kasaian, Marion
; APPLICANT: Wood, Nancy L.

; APPLICANT: Donaldson, Debra D.
; APPLICANT: Collins, Mary
; TITLE OF INVENTION: MODULATION OF IMMUNOGLOBULIN PRODUCTION AND ATOPIC DISORDERS
; FILE REFERENCE: 16158-016W01
; CURRENT APPLICATION NUMBER: PCT/US05/17514
; CURRENT FILING DATE: 2005-05-24
; PRIOR APPLICATION NUMBER: US 60/572,407
; PRIOR FILING DATE: 2004-05-19
; NUMBER OF SEQ ID NOS: 12
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 8
; LENGTH: 529
; TYPE: PRT
; ORGANISM: Mus musculus
PCT-US05-17514-8

Query Match 58.7%; Score 1735.5; DB 1; Length 529;
Best Local Similarity 62.7%; Pred. No. 1.2e-114;
Matches 340; Conservative 49; Mismatches 136; Indels 17; Gaps 6;

QY 1 MPRGWAAPLLLLLQGGGCPDLVCYTDYQVVICILEMNNLHPSTLTLTWQDQVEELKD 60
DB 1 MPRGWAAPLLLLLQGGGCPDLVCYTDYQVVICILEMNNLHPSTLTLTWQDQVEELKD 60

QY 61 EATCSLHRSAHNATHATYTCMDVHFHMADDIFSVNITDQSGNYSQBCSFLLAESIKP 120
DB 61 EATCSLHRSAHNATHATYTCMDVHFHMADDIFSVNITDQSGNYSQBCSFLLAESIKP 120

QY 121 APPFNVTTFSGQYNISWRSDYEDPAFYMLKGKQYELQYRNRPDPWAVSPRRKLIISVDS 180
DB 121 APPFNVTTFSGQYNISWRSDYEDPAFYMLKGKQYELQYRNRPDPWAVSPRRKLIISVDS 180

QY 181 RSVLLPLEFRKDSYELQVRAGPMGSSYQGTWSEWSDPVI FQTSBELKEGWNPHLL 240
DB 181 RSVLLPLEFRKDSYELQVRAGPMGSSYQGTWSEWSDPVI FQTSBELKEGWNPHLL 240

QY 241 LLLLIVVIFAPFWSLTKTHPLWRLMKKIWA VPSPERFMPLYKGCSDGFKWVGAPFTGSS 299
DB 241 LLLLIVVIFAPFWSLTKTHPLWRLMKKIWA VPSPERFMPLYKGCSDGFKWVGAPFTGSS 299

QY 300 SLELGWSPEVPTLEVYSCHPSPSPAKRLQLTLEQPAELVESDGVKPSFVWPTAQN 356
DB 300 SLELGWSPEVPTLEVYSCHPSPSPAKRLQLTLEQPAELVESDGVKPSFVWPTAQN 354

QY 357 NSGSAYSEERDRPYGLVSDITVTVLDAEGCTWPCSCDDGYPALDLDAGLEPSGLD 416
DB 355 GQAVSAYSEERDRPYGLVSDITVTVLDAEGCTWPCSCDDGYPALDLDAGLEPSGLD 414

QY 417 PLLDAGTTVLSCGVSAGSFGGLGSLDLRLKPLPADGEDWAGGLPWGGRSPGCVSE 476
DB 415 LLLVTDPAFLSCGVSAGSFGGLGSLDLRLKPLPADGEDWAGGLPWGGRSPGCVSE 474

QY 477 EAGSPLAGLMDTDFSGFVSGSDCSSPVECDFTSPGDEGPPRSYLRQWVIPPPLSSPGQ 536
DB 475 EAGSP-PLGMDTDFSGFVSGSDCSSPVECDFTSPGDEGPPRSYLRQWVIPPPLSSPGQ 527

QY 537 AS 538
DB 528 SS 529

RESULT 6

US-11-132-947-8
; Sequence 8, Application US/11132947
; GENERAL INFORMATION:
; APPLICANT: Kasaian, Marion
; APPLICANT: Wood, Nancy L.
; APPLICANT: Donaldson, Debra D.
; APPLICANT: Collins, Mary
; TITLE OF INVENTION: MODULATION OF IMMUNOGLOBULIN PRODUCTION AND ATOPIC DISORDERS
; FILE REFERENCE: 16158-016001
; CURRENT APPLICATION NUMBER: US/11/132,947
; CURRENT FILING DATE: 2005-05-19

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; PRIOR APPLICATION NUMBER: US 60/572,407
; FILING DATE: 2004-05-19
; NUMBER OF SEQ ID NOS: 12
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 8
; LENGTH: 529
; TYPE: PRT
; ORGANISM: Mus musculus
US-11-132-947-8

Query Match      58.7%; Score 1735.5; DB 7; Length 529;
Best Local Similarity 62.7%; Pred. No. 1.2e-114;
Matches 340; Conservative 49; Mismatches 136; Indels 17; Gaps 6;

Qy 1 MPRGWAAPLLLLLQGGGCPDLVCYTDYLTQVTCILEMNLHPSTLTLTWQDQYEELKD 60
Db 1 MPRGWAAPLLLLLQGGGCPDLVCYTDYLTQVTCILEMNLHPSTLTLTWQDQYEELKD 60

Qy 61 EATCSLHRSAHNATHATYTCCHMDVHFHMAADDIPFVNITDQSGNYSQECGSFLLAESIKP 120
Db 61 QETFCSLHRSAGHNTTHIWTCHMRLSQFLSDEVFVNVVTDQSGNNSQECGSFVLAESIKP 120

Qy 121 APPENVTVTFSGQYNISWRSDYEDPAFYMLKGKIQYELQYRNRGDPWAVSPRRKLISVDS 180
Db 121 APPENVTVTFSGQYNISWRSDYEDPAFYMLKGKIQYELQYRNRGDPWAVSPRRKLISVDS 180

Qy 181 RSVSLLPLEFRKQSSYELQVRAGMPGSSYQGTWSEWSDPVIQTQSEELKEGWNPH 237
Db 181 RSVSLLPLEFRKQSSYELQVRAGMPGSSYQGTWSEWSDPVIQTQSEELKEGWNPH 237

RESULT 8
US-11-075-351-32
; Sequence 32, Application US/11075351
; GENERAL INFORMATION:
; APPLICANT: Moore, Margaret D.
; APPLICANT: Fox, Brian A.
; TITLE OF INVENTION: DIMERIC FUSION PROTEINS AND MATERIALS
; FILE REFERENCE: 02-16
; CURRENT APPLICATION NUMBER: US/11/075,351
; CURRENT FILING DATE: 2005-03-08
; NUMBER OF SEQ ID NOS: 63
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 32
; LENGTH: 384
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: fusion protein
US-11-075-351-32

Query Match      44.0%; Score 1302; DB 7; Length 384;
Best Local Similarity 100.0%; Pred. No. 3.6e-84;
Matches 237; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MPRGWAAPLLLLLQGGGCPDLVCYTDYLTQVTCILEMNLHPSTLTLTWQDQYEELKD 60
Db 1 MPRGWAAPLLLLLQGGGCPDLVCYTDYLTQVTCILEMNLHPSTLTLTWQDQYEELKD 60

Qy 61 EATCSLHRSAHNATHATYTCCHMDVHFHMAADDIPFVNITDQSGNYSQECGSFLLAESIKP 120
Db 61 EATCSLHRSAHNATHATYTCCHMDVHFHMAADDIPFVNITDQSGNYSQECGSFLLAESIKP 120

Qy 121 APPENVTVTFSGQYNISWRSDYEDPAFYMLKGKIQYELQYRNRGDPWAVSPRRKLISVDS 180
Db 121 APPENVTVTFSGQYNISWRSDYEDPAFYMLKGKIQYELQYRNRGDPWAVSPRRKLISVDS 180

Qy 181 RSVSLLPLEFRKQSSYELQVRAGMPGSSYQGTWSEWSDPVIQTQSEELKEGWNPH 237
Db 181 RSVSLLPLEFRKQSSYELQVRAGMPGSSYQGTWSEWSDPVIQTQSEELKEGWNPH 237

RESULT 9
PCT-US03-10870-439
; Sequence 439, Application PC/TUS0310870
; GENERAL INFORMATION:
; APPLICANT: Mitokor, Inc.
; APPLICANT: Buck Institute
; APPLICANT: Ghosh, Soumitra S.
; APPLICANT: Fahy, Eoin D.

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; APPLICANT: Zhang, Bing
; APPLICANT: Gibson, Bradford W.
; APPLICANT: Taylor, Steven W.
; APPLICANT: Glenn, Gary M.
; APPLICANT: Warnock, Dale E.
; TITLE OF INVENTION: TARGETS FOR THERAPEUTIC INTERVENTION
; TITLE OF INVENTION: IDENTIFIED IN THE MITOCHONDRIAL PROTEOME
; FILE REFERENCE: 660088.465PC
; CURRENT APPLICATION NUMBER: PCT/US03/10870
; CURRENT FILING DATE: 2003-04-04
; NUMBER OF SEQ ID NOS: 3025
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 439
; LENGTH: 551
; TYPE: PRT
; ORGANISM: Homo sapiens
PCT-US03-10870-439

Query Match          9.4%; Score 278; DB 1; Length 551;
Best Local Similarity 26.0%; Pred. No. 1.5e-11;
Matches 137; Conservative 75; Mismatches 199; Indels 116; Gaps 31;

QY 5 WAAPIILL--LQGGW-----GCPDLVCYTDYLTQVICILEMNLHPSTLTLTWQDOVE 56
Db 8 WRLPILLILLPLATSWASAAVNGTSQFTCFYNSRANISCV---WS-----QDQ 52

QY 57 ELKDEATSCSLH-----RSAHNAT-----HATYTCNM-----DVHFMAADDIFSNTID 100
Db 53 ALQD--TSCQVHAMPDRRRWNTCELLPVSAQSWACNLILGAPDSQKLTITVDIVTLRLVC 110

QY 101 QSGNYSQECG--SFLLAESIKAPPNVTVP--SGQVNIWSRSDYEDPAFVMLKGLQY 156
Db 111 REGVRWVMAIQDFKPFENLRMAPISLQVVHVHETHRCNISWEI---SQASHYFERHLEF 167

QY 157 ELQYRNRGDPWAVSPRRKLIISVDSRSVLLPLEFRKDSSEYELQVRAGMPGSSYQGTWSE 216
Db 168 EARTLSPGHTWEAP---LLTLKQEWICLETLPDQYEFQVRVKPLQGEF--TTWSP 222

QY 217 WSDPVIFQTSBELKEG---WNPHLLILLLVIVIFAPFWSL-----KTHPLWRLW-KKIW 268
Db 223 WSQPLAFRTKPAALGKDTIPWLGHLVGLSGAFGIILVYLLINCRNTGP---WLKKVL 278

QY 269 A--VSPERPFMPLYKGCSDGFKKVGAPPTGSSLELGPWSPPEVSTLEVYSCHPRSPA 326
Db 279 KCNTPDPSKFFSQLSSEHGSDVQKWLSSFPSPSSFGGLAPEI-SPLEV-----L 328

QY 327 KRLQLTQLQEPALVESDGVKPSFWPTAQNSSGSAVSEERDRPYGLVSIIDTVTLDAEG 386
Db 329 ERDKVTQL-----LQODKVPEPA-----SLSNHSLTSCFTNQGYFFPHLPDALEIEA-- 377

QY 387 PC-----TWPCSCDD-----GYPALDLDAGLESPGLEPDLDDAGTTVLSCGCVSAGSP 436
Db 378 -CQVYFTYDPYSEEDPDGAVAGAPTSSPQPLQPSG-ED---DAYCTFPSPRDDLLFLSP 432

QY 437 G-LGSP-----LGSLLDRLKPLAD--GEDWAGGLPWGGRSPG 471
Db 433 SLLGSPSPSTAPGSGAGEERMPPLQERVPRDW-DPQLPGPPTPG 478

RESULT 11
US-60-685-372-1266
; Sequence 1266, Application US/60685372
; GENERAL INFORMATION:
; APPLICANT: Belouchi, Abdelmajid
; APPLICANT: Raelson, John V
; APPLICANT: Bradley, Walter E
; APPLICANT: Paquin, Bruno
; APPLICANT: Nguyen-Huu, Quynh
; APPLICANT: Croteau, Pascal
; APPLICANT: Allard, Rene
; APPLICANT: Little, Randall D
; APPLICANT: Cousineau, Johanne
; APPLICANT: Eerdewegh, Paul V
; APPLICANT: Segal, Jonathan
; TITLE OF INVENTION: GeneMap of the Human Genes Associated with Psoriasis
; FILE REFERENCE: 059908-5005-PR
; CURRENT APPLICATION NUMBER: US/60/685,372
; CURRENT FILING DATE: 2005-05-31
; NUMBER OF SEQ ID NOS: 2738
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 1266
; LENGTH: 551
; TYPE: PRT
; ORGANISM: Homo sapiens

; APPLICANT: Zhang, Bing
; APPLICANT: Gibson, Bradford W.
; APPLICANT: Taylor, Steven W.
; APPLICANT: Glenn, Gary M.
; APPLICANT: Warnock, Dale E.
; TITLE OF INVENTION: TARGETS FOR THERAPEUTIC INTERVENTION
; TITLE OF INVENTION: IDENTIFIED IN THE MITOCHONDRIAL PROTEOME
; FILE REFERENCE: 660088.465PC
; CURRENT APPLICATION NUMBER: PCT/US03/10870
; CURRENT FILING DATE: 2003-04-04
; NUMBER OF SEQ ID NOS: 3025
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 439
; LENGTH: 551
; TYPE: PRT
; ORGANISM: Homo sapiens
PCT-US03-10870-439

Query Match          9.4%; Score 278; DB 1; Length 551;
Best Local Similarity 26.0%; Pred. No. 1.5e-11;
Matches 137; Conservative 75; Mismatches 199; Indels 116; Gaps 31;

QY 5 WAAPIILL--LQGGW-----GCPDLVCYTDYLTQVICILEMNLHPSTLTLTWQDOVE 56
Db 8 WRLPILLILLPLATSWASAAVNGTSQFTCFYNSRANISCV---WS-----QDQ 52

QY 57 ELKDEATSCSLH-----RSAHNAT-----HATYTCNM-----DVHFMAADDIFSNTID 100
Db 53 ALQD--TSCQVHAMPDRRRWNTCELLPVSAQSWACNLILGAPDSQKLTITVDIVTLRLVC 110

QY 101 QSGNYSQECG--SFLLAESIKAPPNVTVP--SGQVNIWSRSDYEDPAFVMLKGLQY 156
Db 111 REGVRWVMAIQDFKPFENLRMAPISLQVVHVHETHRCNISWEI---SQASHYFERHLEF 167

QY 157 ELQYRNRGDPWAVSPRRKLIISVDSRSVLLPLEFRKDSSEYELQVRAGMPGSSYQGTWSE 216
Db 168 EARTLSPGHTWEAP---LLTLKQEWICLETLPDQYEFQVRVKPLQGEF--TTWSP 222

QY 217 WSDPVIFQTSBELKEG---WNPHLLILLLVIVIFAPFWSL-----KTHPLWRLW-KKIW 268
Db 223 WSQPLAFRTKPAALGKDTIPWLGHLVGLSGAFGIILVYLLINCRNTGP---WLKKVL 278

QY 269 A--VSPERPFMPLYKGCSDGFKKVGAPPTGSSLELGPWSPPEVSTLEVYSCHPRSPA 326
Db 279 KCNTPDPSKFFSQLSSEHGSDVQKWLSSFPSPSSFGGLAPEI-SPLEV-----L 328

QY 327 KRLQLTQLQEPALVESDGVKPSFWPTAQNSSGSAVSEERDRPYGLVSIIDTVTLDAEG 386
Db 329 ERDKVTQL-----LQODKVPEPA-----SLSNHSLTSCFTNQGYFFPHLPDALEIEA-- 377

QY 387 PC-----TWPCSCDD-----GYPALDLDAGLESPGLEPDLDDAGTTVLSCGCVSAGSP 436
Db 378 -CQVYFTYDPYSEEDPDGAVAGAPTSSPQPLQPSG-ED---DAYCTFPSPRDDLLFLSP 432

QY 437 G-LGSP-----LGSLLDRLKPLAD--GEDWAGGLPWGGRSPG 471
Db 433 SLLGSPSPSTAPGSGAGEERMPPLQERVPRDW-DPQLPGPPTPG 478

RESULT 10
US-11-033-545-308
; Sequence 308, Application US/11033545
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; TITLE OF INVENTION: WITH INFLAMMATORY AUTOIMMUNE DISEASE, METHODS OF DETECTION
; TITLE OF INVENTION: AND USES THEREOF
; FILE REFERENCE: CL000790
; CURRENT APPLICATION NUMBER: US/11/033,545
; CURRENT FILING DATE: 2005-01-12
; PRIOR APPLICATION NUMBER: 60/231,401
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 10823
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US-60-685-372-1266

```
Query Match          9.4%; Score 278; DB 8; Length 551;
Best Local Similarity 26.0%; Pred. No. 1.5e-11;
Matches 137; Conservative 75; Mismatches 199; Indels 116; Gaps 31;

QY 5 WAAPLLILL--LQGGW-----GCPDLVCYTDYLTQVICILEMNLHPSTLTLTWQDOYE 56
DB 8 WRLPLLILLPLATWSAAVNGTSQFTCFYNSRANISCV---WS-----QDG 52

QY 57 ELKDEATSCSLH-----RSAHNA-----HATYTCM-----DVHFMAADIFSVNITD 100
DB 53 ALQD--TSCQVHAWPDRRRWQTCFYNLRMAPISLQVHVHETHRCNISWEI---SQASHYFERHLEF 110

QY 101 QSGNYSQEG--SPLLAESIKPAPPFNVTYTF--SGQYNISWRSDYEDPAFYMKGKLOY 156
DB 111 REGVRWRVMAIQDPKPFENLRMAPISLQVHVHETHRCNISWEI---SQASHYFERHLEF 167

QY 157 ELOYRNRGDPWAVSPRRKLISVDRSVSLPLLEFRKDSSEYELQVRAGMPGSSYQGTWSE 216
DB 168 EARTLSFGHTWEEAP---LLTLKQKQEWICLETTLPTDQYEFQVRVKPLOGEF--TTWSP 222

QY 217 WSDPVIQFOTQSEELKEG---WNPHLLLLLLLVIFIPAFWSL-----KTHPLWRLW-KKIW 268
DB 223 WSQPLAFRTKPAALGKDTIPWLGHLVGLSGAFGIILVYLLINCRNTGP-----WLKKVL 278

QY 269 A--VPSPERFMPYKCGSGDFKWKVGAFTGSSLSLELGPWSPVSTLEVYVCHPPRSPA 326
DB 279 KNTNPDPSKFFQSLSSEHGVDQVKWLSPPSSPSSPGLAPEI-SPLEV-----L 328

QY 327 KRLQLTQELQPAELVESDGVKPSFWPTAQNSGGSAYSSEERDRPYGLVSIIDTVTLDAEG 386
DB 329 ERDKVTQL-----LQQDKVPEPA-----SLSNHSLTSCFTNQGYFFPHLPDALEIEA-- 377

QY 387 PC-----TWPSCEDD-----GYPALDLDAGLESPGLEPDLDDAGTTVLSCGCVSAGSP 436
DB 378 -CQVYFTYDPYSEEDPDGAVAGAPTGSPPQLPLSG-ED---DAYCTFPSRDDLLLFSP 432

QY 437 G-LGGP-----LGSLLDLRLKPLAD--GEDWAGGLPWGGRSPG 471
DB 433 SLLGGPSPSTAPGGSGAGEERMPPLQERVRPDW-DPQPLGPPPTG 478

RESULT 12
US-11-033-545-537
; Sequence 537, Application US/11033545
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; WITH INFLAMMATORY AUTOIMMUNE DISEASE, METHODS OF DETECTION
; TITLE OF INVENTION: AND USES THEREOF
; FILE REFERENCE: CL000790
; CURRENT APPLICATION NUMBER: US/11/033,545
; CURRENT FILING DATE: 2005-01-12
; PRIOR APPLICATION NUMBER: 60/231,401
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 10823
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 537
; LENGTH: 594
; TYPE: PRT
; ORGANISM: Human
US-11-033-545-537

Query Match          9.4%; Score 278; DB 7; Length 594;
Best Local Similarity 26.0%; Pred. No. 1.6e-11;
Matches 137; Conservative 75; Mismatches 199; Indels 116; Gaps 31;

QY 5 WAAPLLILL--LQGGW-----GCPDLVCYTDYLTQVICILEMNLHPSTLTLTWQDOYE 56
DB 51 WRLPLLILLPLATWSAAVNGTSQFTCFYNSRANISCV---WS-----QDG 95

QY 57 ELKDEATSCSLH-----RSAHNA-----HATYTCM-----DVHFMAADIFSVNITD 100
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DB 96 ALQD--TSCQVHAWPDRRRWQTCFYNLRMAPISLQVHVHETHRCNISWEI---SQASHYFERHLEF 153
QY 101 QSGNYSQEG--SPLLAESIKPAPPFNVTYTF--SGQYNISWRSDYEDPAFYMKGKLOY 156
DB 154 REGVRWRVMAIQDPKPFENLRMAPISLQVHVHETHRCNISWEI---SQASHYFERHLEF 210
QY 157 ELOYRNRGDPWAVSPRRKLISVDRSVSLPLLEFRKDSSEYELQVRAGMPGSSYQGTWSE 216
DB 211 EARTLSFGHTWEEAP---LLTLKQKQEWICLETTLPTDQYEFQVRVKPLOGEF--TTWSP 265
QY 217 WSDPVIQFOTQSEELKEG---WNPHLLLLLLLVIFIPAFWSL-----KTHPLWRLW-KKIW 268
DB 266 WSQPLAFRTKPAALGKDTIPWLGHLVGLSGAFGIILVYLLINCRNTGP-----WLKKVL 321
QY 269 A--VPSPERFMPYKCGSGDFKWKVGAFTGSSLSLELGPWSPVSTLEVYVCHPPRSPA 326
DB 322 KNTNPDPSKFFQSLSSEHGVDQVKWLSPPSSPSSPGLAPEI-SPLEV-----L 371
QY 327 KRLQLTQELQPAELVESDGVKPSFWPTAQNSGGSAYSSEERDRPYGLVSIIDTVTLDAEG 386
DB 372 ERDKVTQL-----LQQDKVPEPA-----SLSNHSLTSCFTNQGYFFPHLPDALEIEA-- 420
QY 387 PC-----TWPSCEDD-----GYPALDLDAGLESPGLEPDLDDAGTTVLSCGCVSAGSP 436
DB 421 -CQVYFTYDPYSEEDPDGAVAGAPTGSPPQLPLSG-ED---DAYCTFPSRDDLLLFSP 475
QY 437 G-LGGP-----LGSLLDLRLKPLAD--GEDWAGGLPWGGRSPG 471
DB 476 SLLGGPSPSTAPGGSGAGEERMPPLQERVRPDW-DPQPLGPPPTG 521
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RESULT 13

```
US-11-021-951-151
; Sequence 151, Application US/11021951
; GENERAL INFORMATION:
; APPLICANT: HAUPTS, Ulrich
; APPLICANT: SCHEIDIG, Andreas
; APPLICANT: VOTSMER, Christian
; APPLICANT: Kettling, Ulrich
; APPLICANT: COCO, Wayne Michael
; TITLE OF INVENTION: New Biological Entities And The Pharmaceutical
; FILE REFERENCE: 04156.0002U5
; CURRENT APPLICATION NUMBER: US/11/021,951
; CURRENT FILING DATE: 2004-12-22
; PRIOR APPLICATION NUMBER: 10/872,198
; PRIOR FILING DATE: 2004-06-18
; PRIOR APPLICATION NUMBER: 60/543,518
; PRIOR FILING DATE: 2004-02-11
; PRIOR APPLICATION NUMBER: 60/524,960
; PRIOR FILING DATE: 2003-11-25
; PRIOR APPLICATION NUMBER: EP 040003058
; PRIOR FILING DATE: 2004-02-11
; PRIOR APPLICATION NUMBER: EP 03025871
; PRIOR FILING DATE: 2003-11-11
; PRIOR APPLICATION NUMBER: EP 03025851
; PRIOR FILING DATE: 2003-11-10
; PRIOR APPLICATION NUMBER: EP 03013819
; PRIOR FILING DATE: 2003-06-18
; NUMBER OF SEQ ID NOS: 191
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 151
; LENGTH: 525
; TYPE: PRT
; ORGANISM: Homo sapiens
US-11-021-951-151
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Query Match          8.7%; Score 256; DB 7; Length 525;
Best Local Similarity 25.5%; Pred. No. 5e-10;
Matches 129; Conservative 74; Mismatches 194; Indels 108; Gaps 29;
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QY 19 GCPDLVCYDYLTQVTCILEMNLHPSTLTLTWQDYBELKDEATSCSLH-----BSAHNA 74
Db 4 GTSQFTCFYNSRANISCV-----WS-----ODGALQD--TSCQVHAMPDRRRMNQ 46
QY 75 T-----HATYTCM-----DVHFPMADDIFSUNITQSGNYSQECG--SELLAESIKP 120
Db 47 TCELLPVSAQWACNLLIGAPDSQKLTVDIVTLVLCREGVWRVMAIQDFKPFENLRL 106
QY 121 APPFNVTVP--SGQYNISWRSDYEDPAPYMLKGLQYELQYLRNRGDPMAVSPRRKLISV 178
Db 107 MAPISLQVHVHETHRCNISWEI---SQASHYFERHLEFEARTLSPGHTWEEAP--LLTL 160
QY 179 DRSVSLLPLERKSSYELQYLRAGMPGSSVQCTWSESDVIFQTOSEELKEG---WN 235
Db 161 KQKQEWICLETPTDQYFQVRVPLQGEF--TWSWMSQPLAFRTKPAALGKDTIPWL 218
QY 236 PHLLLLLLVIVIFAPFMSL-----KTHPLRLW--KKIWA--VPSPERFFMPLYKGCSDG 288
Db 219 GHLVCLSGAFGFIILVILLINCRNTP-----WLKVKLCNTPDPSKFSQSSSEHGDDV 274
QY 289 KKWVGAPFTGSSLELGPMSPEVPSTLEVYSCHPSPRAKRLQTLQELQEPALVESDGVPK 348
Db 275 QKWLSPPSPSSFSFGGLAPEI--SPLEV-----LERDKVTQL-----LLQDQKVE 319
QY 349 PSFWPTAONGSGSAYSEERDRPYGLVSDTVTLDAEGPC-----TWPCSCDD-----G 398
Db 320 PA-----SUSSNHSLSCTFNOGYFFPHLPDALEIEA---CQVYFTYDPYSEEDPDGVAG 372
QY 399 YPALDLDALESPGLEPDLDTLSCGCVSAGSP--LGPP-----LGSLLDR 448
Db 373 ATGSSPQLPLSG--ED---DAYCTFPRDRDILLFSPSLLGPPSPPTAPGSGAGER 428
QY 449 LKPIPLAD--GEDWAGGLPMGRSPG 471
Db 429 MPESLQERVPRDW--DQPLGPPTG 452

RESULT 14
US-10-940-774A-8560
; Sequence 8560, Application US/10940774A
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/10/940,774A
; CURRENT FILING DATE: 2004-09-15
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 8560
; LENGTH: 536
; TYPE: PRT
; ORGANISM: Human
US-10-940-774A-8560

Query Match 7.8%; Score 231; DB 6; Length 536;
Best Local Similarity 25.2%; Pred. No. 3e-08;
Matches 143; Conservative 53; Mismatches 206; Indels 166; Gaps 34;

QY 17 GNGCPDLVCYDYLTQVTCILEMNLHPSTLTLTWQDYBELKDEATSC-----65
Db 8 GNGCLRLV-----MGLGRCIWEGWLTSEALRDMGTW-----LLACICICTVCV 52
QY 66 ---SLHRSAHNATHATYTC-----HMDVFHFMADD-----IFSVNITDQSGNY-- 105
Db 53 LGVSVTGEQGRSRFTTCLTNILRIDC--HWSAPELGGSSPFWLLFTSN--QAPCGTHKC 110

QY 106 ---SQECGSFLLAESIKPAPPFNVTVP-----SGQYNISW-----RSDYE 143
Db 111 ILRGSECTVLPPEAVL--VPSDNFTITTHCMCSGREQVSLVDPPEYLPRRHVKLDPSPDLQ 169
QY 144 -----DPAFYMLKGLQYELQYLRNRGDPMAVSPRRKLISVDSRSVSLPLLE 189
Db 170 SNISSGHCILTWSISPALLEPMTLLSYELAFKKQEEAMEQAHRDHIV-----GVTWLILUE 225
QY 190 -FRKDSSY-----ELQVRAGMPG-----SSYOGTWSESDVIFQTOSEEE-----LKEGWN 235
Db 226 APELDPGFIHEARLRVQMATLEDDVVEBERYTQGWSEWSQVCFQAPQRCQGLIPFWGWP 285
QY 236 PHLLLLLLVIVIFAPFMSLATHPLRLW-----KKIWA--AVPSPERFFMPLYKGCSD 287
Db 286 GN---TLVAVSIFL-----LITGPTYLLFLKLSPRVKRIFYQNVPSAMFFQPLYSVHNGN 337
QY 288 FKWVGAPFTGSSLE-----LGWSPSEVPSTLEVYSCHPSPRAKRLQTLQELQE----- 336
Db 338 QOTWGAHAGAGVILLSQDCAGTPOGNALEFCVQEAETALLTCGPAP--PWKSVALEEEGEGPCT 396
QY 337 --PAELVESDGVKPSFWPTAONGSGSAYSEERDRPYGLVSDTVTLDAEG--PCTWPC 392
Db 397 RLPGNLSSSEDVLPAGC---TEWRVQTLAYLPQED--WAPTSLTRPAPDPDSEGRSSSSSS 451
QY 393 SCEDDGYPALDLDAAG--LEPSPGLE-----PLLDAGTTVLSC-----CCVSAG 434
Db 452 SNNNNYCALQCYGCGHLSALPGNTQSSGPIPALACG---LSCDHQGLETOQGVAVMLAG 508
QY 435 ---SPGLGGLGSLDLRLKPLADGEDW 459
Db 509 HCQRPGLHEDLQGLM--LPSVLKXRSW 534

Query Match 7.4%; Score 219.5; DB 1; Length 823;
Best Local Similarity 22.3%; Pred. No. 3.4e-07;
Matches 142; Conservative 67; Mismatches 221; Indels 207; Gaps 35;

QY 17 GNGCPDLV-----CYTDYLTQVTCILEMNL--HPST-----L 47
Db 2 GMLCSGLTFPVSCVLVWVASSGSVKVLHBFSCFSDYSTVC---QMKMDHPITNCSAEL 58
QY 48 TLTWQDYBELKDEATSCSLHRSAHNATHATYTCMVHFHMADDIFSUNITDQSGNSQ 107
Db 59 RLSYQLDF--MGSENHTC---VPERNREDSVCVCSMPIDDAVEADYQLDL--WAGQQLL 110
QY 108 ECGSFLLAESIKPAPPFNVTVP--TFSGQYNISWRSDYEDPAPYMLKGLQYELQYLRNGD 165
Db 111 WSGSFQPSKHKVPRTPGNTLVHPNISHTWLLMWTNPFY--PTENHLHSELTYMVNVNSND 168

RESULT 15
PCT-US04-17028-11
; Sequence 11, Application PC/TUS0417028
; GENERAL INFORMATION:
; APPLICANT: Watson, Johanna L.
; APPLICANT: Jackson, Kenneth A.
; APPLICANT: The Regents of the University of California
; TITLE OF INVENTION: IL4 Receptor Antagonists for Horse, Dog and Cat
; FILE REFERENCE: 023070-133820PC
; CURRENT APPLICATION NUMBER: PCT/US04/17028
; CURRENT FILING DATE: 2004-05-28
; PRIOR APPLICATION NUMBER: US 60/475,220
; PRIOR FILING DATE: 2003-05-30
; PRIOR APPLICATION NUMBER: US 60/561,579
; PRIOR FILING DATE: 2004-04-12
; NUMBER OF SEQ ID NOS: 48
; SOFTWARE: Patent In Ver. 2.1
; SEQ ID NO 11
; LENGTH: 823
; TYPE: PRT
; ORGANISM: Canis familiaris
; FEATURE:
; OTHER INFORMATION: dog interleukin-4 (IL4) receptor (IL4R)
PCT-US04-17028-11

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QY 166 PWAVSPREKLJSD--SRVSILLPLERKSSYELQVRAGPMPGSSYQGTWSEWSDPVP 223
Db 169 P-----EDFKVTNVTMGFTLRLAASTLKSAGSYARVRW--AQTYNSTWSDNSP---- 217
QY 224 QTQSEELKEGWNPHLL-----LLLLVIVFIPAFWSLKTHTPLWRLWKKIWAVPSP---- 273
Db 218 STRWLNYYPWEQHLPLGVISLCLVLAICLCYFSIIKIKKGW--WDQI---ENPAHSP 272
QY 274 -----ERFMPLYKGC-----SGDFKKWVGAPFTGSSLEL 303
Db 273 LVAVIODSQVSLWGRSRGQEPAPKCPHWKCTLTKLLPCLLEHGLGREESPKTAKNGPL 332
QY 304 -GP-----WSP-EV-----PSTLEVYSCHPPRSPAKRLQLTEL---QEPaelVESDGVPK 348
Db 333 QOPGKPAWCPVEVSKTILWPESISVVQC-----VELSEAPVDNEEEVEED---K 380
QY 349 PSFWPTAQNGSGSAYSEERDRPYGLVSIIDTVTV-LDAEGPCTWPCSCDDGYPALDLDA 407
Db 381 RSLCFSLGSGGS-FQEGRE--GIVARLTESLFLDLIG-----ENGFCFCQGLEES 429
QY 408 LEPSFGLDPLLDAGTTVLSCGVSAGSPGLGGPLGSLDLRLKPLADGEDWAGGLPWGG 467
Db 430 CLPPPS-----GSVGAQMPWAQFP-----RAGPRAA-----PEGP 459
QY 468 RSPGVSESEAGSPLAGLMDTF-----DSGFVGSDD---CS 500
Db 460 EQPRRPSALQASPTQASGSAFEPPEPPVVTNDNPAYRSFGSFLGSSDPGSDSDPELAD 519
QY 501 SPVECDFTSPGDEGPPRSYLRQWVVI PPPPLSSPGFQA 537
Db 520 RPGEADPGIPSAPQPE-----PPAALQPREPES 547
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Search completed: July 9, 2005, 11:57:52
Job time : 66 secs

GenCore version 5.1.1.6
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OM protein - protein search, using sw model
Run on: July 9, 2005, 11:41:15 ; Search time 475 Seconds
(without alignments)
1322.921 Million cell updates/sec

Title: US-10-620-169-4
Perfect score: 2958
Sequence: 1 MPRGWAAPLILLLLQLGGWGC.....YLRQWVIPPPLSSPGPOAS 538

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 6959266 seqs, 1168006243 residues

Total number of hits satisfying chosen parameters: 6959266

Minimum DB seq length: 0
Maximum DB seq length: 2000000000
Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

- Database :
- 1: /cgn2_6/ptodata/1/paa/PCTUS COMB.pcp.*
 - 2: /cgn2_6/ptodata/1/paa/US06_COMB.pcp.*
 - 3: /cgn2_6/ptodata/1/paa/US07_COMB.pcp.*
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 - 5: /cgn2_6/ptodata/1/paa/US081 COMB.pcp.*
 - 6: /cgn2_6/ptodata/1/paa/US082 COMB.pcp.*
 - 7: /cgn2_6/ptodata/1/paa/US083 COMB.pcp.*
 - 8: /cgn2_6/ptodata/1/paa/US084 COMB.pcp.*
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 - 11: /cgn2_6/ptodata/1/paa/US087 COMB.pcp.*
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 - 22: /cgn2_6/ptodata/1/paa/US097B COMB.pcp.*
 - 23: /cgn2_6/ptodata/1/paa/US098 COMB.pcp.*
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 - 25: /cgn2_6/ptodata/1/paa/US099B COMB.pcp.*
 - 26: /cgn2_6/ptodata/1/paa/US100 COMB.pcp.*
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 - 36: /cgn2_6/ptodata/1/paa/US110 COMB.pcp.*
 - 37: /cgn2_6/ptodata/1/paa/US60_COMB.pcp.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB	ID	Description
1	2958	100.0	538	1	PCT-US00-06067-115	Sequence 115, Appli
2	2958	100.0	538	1	PCT-US00-13687-2	Sequence 2, Appli
3	2958	100.0	538	1	PCT-US02-29839-2	Sequence 2, Appli
4	2958	100.0	538	1	PCT-US02-34502-16	Sequence 16, Appli
5	2958	100.0	538	1	PCT-US03-17808-6	Sequence 6, Appli
6	2958	100.0	538	1	PCT-US03-21975-4	Sequence 4, Appli
7	2958	100.0	538	1	PCT-US04-08833-6	Sequence 6, Appli
8	2958	100.0	538	15	US-09-159-254-2	Sequence 2, Appli
9	2958	100.0	538	16	US-09-264-908-2	Sequence 2, Appli
10	2958	100.0	538	16	US-09-265-117-2	Sequence 2, Appli
11	2958	100.0	538	17	US-09-313-913-2	Sequence 2, Appli
12	2958	100.0	538	17	US-09-347-930-2	Sequence 2, Appli
13	2958	100.0	538	19	US-09-543-320-2	Sequence 2, Appli
14	2958	100.0	538	19	US-09-560-766-2	Sequence 2, Appli
15	2958	100.0	538	19	US-09-569-384-2	Sequence 2, Appli
16	2958	100.0	538	19	US-09-574-100-2	Sequence 2, Appli
17	2958	100.0	538	20	US-09-628-127-2	Sequence 2, Appli
18	2958	100.0	538	21	US-09-720-285-7	Sequence 7, Appli
19	2958	100.0	538	25	US-09-965-313-2	Sequence 2, Appli
20	2958	100.0	538	25	US-09-972-218A-2	Sequence 2, Appli
21	2958	100.0	538	25	US-09-972-218B-2	Sequence 2, Appli
22	2958	100.0	538	27	US-10-170-205B-23124	Sequence 23124, A
23	2958	100.0	538	28	US-10-264-634-2	Sequence 2, Appli
24	2958	100.0	538	28	US-10-282-622-16	Sequence 16, Appli
25	2958	100.0	538	30	US-10-456-262A-6	Sequence 6, Appli
26	2958	100.0	538	30	US-10-456-780-6	Sequence 6, Appli
27	2958	100.0	538	32	US-10-620-169-4	Sequence 4, Appli
28	2958	100.0	538	32	US-10-659-684-115	Sequence 115, App
29	2958	100.0	538	33	US-10-715-998-2	Sequence 2, Appli
30	2958	100.0	538	33	US-10-787-442-115	Sequence 115, App
31	2958	100.0	538	33	US-10-798-380-43	Sequence 43, Appli
32	2958	100.0	538	34	US-10-806-611-6	Sequence 6, Appli
33	2958	100.0	538	34	US-10-864-249-2	Sequence 2, Appli
34	2958	100.0	538	34	US-10-872-087-2	Sequence 2, Appli
35	2958	100.0	538	35	US-10-951-239-10	Sequence 10, Appli
36	2958	100.0	538	37	US-60-453-050-9170	Sequence 9170, Ap
37	2958	100.0	538	37	US-60-453-135-9170	Sequence 9170, Ap
38	2958	100.0	538	37	US-60-455-444-4984	Sequence 4984, Ap
39	2958	100.0	538	37	US-60-455-241-4984	Sequence 4984, Ap
40	2958	100.0	538	37	US-60-466-412-9170	Sequence 9170, Ap
41	2958	100.0	538	37	US-60-505-919-10	Sequence 10, Appli
42	2958	100.0	547	35	US-10-940-774-11544	Sequence 11544, A
43	2951	99.8	538	1	PCT-US99-25617-2	Sequence 2, Appli
44	2951	99.8	538	15	US-09-187-711-2	Sequence 2, Appli
45	2951	99.8	538	15	US-09-187-711A-2	Sequence 2, Appli

ALIGNMENTS

RESULT 1
PCT-US00-06067-115
; Sequence 115, Application PC/TUS0006067
; GENERAL INFORMATION:
; APPLICANT: ZymoGenetics, Inc.
; TITLE OF INVENTION: NOVEL CYTOKINE ZALPHAL1 LIGAND
; FILE REFERENCE: 99-16PC
; CURRENT APPLICATION NUMBER: PCT/US00/06067
; CURRENT FILING DATE: 2000-03-09
; EARLIER APPLICATION NUMBER: US 09/264,908
; EARLIER FILING DATE: 1999-03-09
; EARLIER APPLICATION NUMBER: US 09/265,992
; EARLIER FILING DATE: 1999-03-11
; EARLIER APPLICATION NUMBER: US 60/142,013
; EARLIER FILING DATE: 1999-07-01
; NUMBER OF SEQ ID NOS: 115
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 115
; LENGTH: 538

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; TYPE: PRT
; ORGANISM: Homo sapiens
PCT-US00-06067-115

Query Match      100.0%; Score 2958; DB 1; Length 538;
Best Local Similarity 100.0%; Pred. No. 1.5e-236;
Matches 538; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MPRGWAAPLLLLLQGGGCPDLVCYTDYLTQVICILEMNNLHPSTLTLTWQDOYEELKD 60
DB 1 MPRGWAAPLLLLLQGGGCPDLVCYTDYLTQVICILEMNNLHPSTLTLTWQDOYEELKD 60

QY 61 EATCSLHRSAHNATHATYTTCHMDVHFHMADDIFSVNITDQSGNYSQCGSFLLAESIKP 120
DB 61 EATCSLHRSAHNATHATYTTCHMDVHFHMADDIFSVNITDQSGNYSQCGSFLLAESIKP 120

QY 121 APPFNVTTFSGQYNIWSRSDYEDPAFYMLKGKQYELQYRNRGDPWAVSPRRKLIISVDS 180
DB 121 APPFNVTTFSGQYNIWSRSDYEDPAFYMLKGKQYELQYRNRGDPWAVSPRRKLIISVDS 180

QY 181 RSVSLLPLEFRKDSSEYELQVRAGMPGSSYQGTWSEWSDPVI FQTQSEELKEGWNPHLLL 240
DB 181 RSVSLLPLEFRKDSSEYELQVRAGMPGSSYQGTWSEWSDPVI FQTQSEELKEGWNPHLLL 240

QY 61 EATCSLHRSAHNATHATYTTCHMDVHFHMADDIFSVNITDQSGNYSQCGSFLLAESIKP 120
DB 61 EATCSLHRSAHNATHATYTTCHMDVHFHMADDIFSVNITDQSGNYSQCGSFLLAESIKP 120

QY 121 APPFNVTTFSGQYNIWSRSDYEDPAFYMLKGKQYELQYRNRGDPWAVSPRRKLIISVDS 180
DB 121 APPFNVTTFSGQYNIWSRSDYEDPAFYMLKGKQYELQYRNRGDPWAVSPRRKLIISVDS 180

QY 181 RSVSLLPLEFRKDSSEYELQVRAGMPGSSYQGTWSEWSDPVI FQTQSEELKEGWNPHLLL 240
DB 181 RSVSLLPLEFRKDSSEYELQVRAGMPGSSYQGTWSEWSDPVI FQTQSEELKEGWNPHLLL 240

QY 241 LLLLIVIFIPAFWSLTKTHPLWRLWKIWA VSPERFFMPLYKGCSDGPKKWWGAPFTGSS 300
DB 241 LLLLIVIFIPAFWSLTKTHPLWRLWKIWA VSPERFFMPLYKGCSDGPKKWWGAPFTGSS 300

QY 301 LELGWPSPVSTLEVYSCHPPRSPAKRLQLTQLQEPAELVESDGVKPKSPFWPTAQNSSG 360
DB 301 LELGWPSPVSTLEVYSCHPPRSPAKRLQLTQLQEPAELVESDGVKPKSPFWPTAQNSSG 360

QY 361 SAYSEERDRPYGLVSIIDVTVLDAEGCTWPCSCDDGYPALDLDAGLEPSPGLEPDL 420
DB 361 SAYSEERDRPYGLVSIIDVTVLDAEGCTWPCSCDDGYPALDLDAGLEPSPGLEPDL 420

QY 421 AGTTVLSGCVSAGSPGLGGPLGSLLDRLKPLADGEDWAGGLPWGGRSPGVSESEAGS 480
DB 421 AGTTVLSGCVSAGSPGLGGPLGSLLDRLKPLADGEDWAGGLPWGGRSPGVSESEAGS 480

QY 481 PLAGLDMDTFDSGFVGCSDSPVECDFTSPGDEGPPRSYLRQWVIPPPLSSPGPQAS 538
DB 481 PLAGLDMDTFDSGFVGCSDSPVECDFTSPGDEGPPRSYLRQWVIPPPLSSPGPQAS 538

RESULT 2
PCT-US00-13687-2
; Sequence 2, Application PC/TUS0013687
; GENERAL INFORMATION:
; APPLICANT: Hodge, Martin R.
; TITLE OF INVENTION: Novel IL-9/IL-2 Receptor-Like Molecules
; FILE REFERENCE: 5800-17A-1
; CURRENT APPLICATION NUMBER: PCT/US00/13687
; PRIOR FILING DATE: 2000-05-18
; PRIOR APPLICATION NUMBER: US 09/313,913
; PRIOR FILING DATE: 1999-05-18
; NUMBER OF SEQ ID NOS: 8
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 2
; LENGTH: 538
; TYPE: PRT
; ORGANISM: Homo sapiens IL-2/IL-9 Receptor Like
PCT-US00-13687-2

Query Match      100.0%; Score 2958; DB 1; Length 538;
Best Local Similarity 100.0%; Pred. No. 1.5e-236;
Matches 538; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MPRGWAAPLLLLLQGGGCPDLVCYTDYLTQVICILEMNNLHPSTLTLTWQDOYEELKD 60
DB 1 MPRGWAAPLLLLLQGGGCPDLVCYTDYLTQVICILEMNNLHPSTLTLTWQDOYEELKD 60

QY 61 EATCSLHRSAHNATHATYTTCHMDVHFHMADDIFSVNITDQSGNYSQCGSFLLAESIKP 120
DB 61 EATCSLHRSAHNATHATYTTCHMDVHFHMADDIFSVNITDQSGNYSQCGSFLLAESIKP 120

QY 121 APPFNVTTFSGQYNIWSRSDYEDPAFYMLKGKQYELQYRNRGDPWAVSPRRKLIISVDS 180
DB 121 APPFNVTTFSGQYNIWSRSDYEDPAFYMLKGKQYELQYRNRGDPWAVSPRRKLIISVDS 180

QY 181 RSVSLLPLEFRKDSSEYELQVRAGMPGSSYQGTWSEWSDPVI FQTQSEELKEGWNPHLLL 240
DB 181 RSVSLLPLEFRKDSSEYELQVRAGMPGSSYQGTWSEWSDPVI FQTQSEELKEGWNPHLLL 240

QY 241 LLLLIVIFIPAFWSLTKTHPLWRLWKIWA VSPERFFMPLYKGCSDGPKKWWGAPFTGSS 300
DB 241 LLLLIVIFIPAFWSLTKTHPLWRLWKIWA VSPERFFMPLYKGCSDGPKKWWGAPFTGSS 300

QY 301 LELGWPSPVSTLEVYSCHPPRSPAKRLQLTQLQEPAELVESDGVKPKSPFWPTAQNSSG 360
DB 301 LELGWPSPVSTLEVYSCHPPRSPAKRLQLTQLQEPAELVESDGVKPKSPFWPTAQNSSG 360

QY 361 SAYSEERDRPYGLVSIIDVTVLDAEGCTWPCSCDDGYPALDLDAGLEPSPGLEPDL 420
DB 361 SAYSEERDRPYGLVSIIDVTVLDAEGCTWPCSCDDGYPALDLDAGLEPSPGLEPDL 420

QY 421 AGTTVLSGCVSAGSPGLGGPLGSLLDRLKPLADGEDWAGGLPWGGRSPGVSESEAGS 480
DB 421 AGTTVLSGCVSAGSPGLGGPLGSLLDRLKPLADGEDWAGGLPWGGRSPGVSESEAGS 480

QY 481 PLAGLDMDTFDSGFVGCSDSPVECDFTSPGDEGPPRSYLRQWVIPPPLSSPGPQAS 538
DB 481 PLAGLDMDTFDSGFVGCSDSPVECDFTSPGDEGPPRSYLRQWVIPPPLSSPGPQAS 538

RESULT 3
PCT-US02-29839-2
; Sequence 2, Application PC/TUS0229839
; GENERAL INFORMATION:
; APPLICANT: Wyeth
; TITLE OF INVENTION: Methods and Composition for Modulating Interleukin-21 Receptor Ac
; FILE REFERENCE: G15320-PCT-P2
; CURRENT APPLICATION NUMBER: PCT/US02/29839
; CURRENT FILING DATE: 2002-10-04
; PRIOR APPLICATION NUMBER: 09/972,218
; PRIOR FILING DATE: 2001-10-04
; NUMBER OF SEQ ID NOS: 44
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 2
; LENGTH: 538
; TYPE: PRT
; ORGANISM: Human
PCT-US02-29839-2

Query Match      100.0%; Score 2958; DB 1; Length 538;
Best Local Similarity 100.0%; Pred. No. 1.5e-236;
Matches 538; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MPRGWAAPLLLLLQGGGCPDLVCYTDYLTQVICILEMNNLHPSTLTLTWQDOYEELKD 60
DB 1 MPRGWAAPLLLLLQGGGCPDLVCYTDYLTQVICILEMNNLHPSTLTLTWQDOYEELKD 60

QY 61 EATCSLHRSAHNATHATYTTCHMDVHFHMADDIFSVNITDQSGNYSQCGSFLLAESIKP 120
DB 61 EATCSLHRSAHNATHATYTTCHMDVHFHMADDIFSVNITDQSGNYSQCGSFLLAESIKP 120

QY 121 APPFNVTTFSGQYNIWSRSDYEDPAFYMLKGKQYELQYRNRGDPWAVSPRRKLIISVDS 180
DB 121 APPFNVTTFSGQYNIWSRSDYEDPAFYMLKGKQYELQYRNRGDPWAVSPRRKLIISVDS 180

QY 181 RSVSLLPLEFRKDSSEYELQVRAGMPGSSYQGTWSEWSDPVI FQTQSEELKEGWNPHLLL 240
DB 181 RSVSLLPLEFRKDSSEYELQVRAGMPGSSYQGTWSEWSDPVI FQTQSEELKEGWNPHLLL 240

QY 241 LLLLIVIFIPAFWSLTKTHPLWRLWKIWA VSPERFFMPLYKGCSDGPKKWWGAPFTGSS 300
DB 241 LLLLIVIFIPAFWSLTKTHPLWRLWKIWA VSPERFFMPLYKGCSDGPKKWWGAPFTGSS 300
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Db 241 LLLLVIVIFAPFWSLKTPLWRLWKIWA VPSPERFPMPLYKCGSDGFKWVGAPFTGSS 300
Qy 301 LELGWPSEVPSTLEVSYCHPPSPAKRLQLTELQEPALVESDGVKPKSPFWPTAQNCGG 360
Db 301 LELGWPSEVPSTLEVSYCHPPSPAKRLQLTELQEPALVESDGVKPKSPFWPTAQNCGG 360
Qy 361 SAYSEERDRPYGLVSDITVTVLDAEGPCTWPCSCEDDGYPALDLDAGLEPSPGLEDPILLD 420
Db 361 SAYSEERDRPYGLVSDITVTVLDAEGPCTWPCSCEDDGYPALDLDAGLEPSPGLEDPILLD 420
Qy 421 AGTTVLSGCGVSAGSPGLGGPLGSLDLRLKPLADGEDWAGGLPWGGRSPGCVSSEAGS 480
Db 421 AGTTVLSGCGVSAGSPGLGGPLGSLDLRLKPLADGEDWAGGLPWGGRSPGCVSSEAGS 480
Qy 481 PLAGLDMDTFDSGFGVSGDCSSPVECDFTSPGDEGPPRSYLRQWVVI PPLSSPGPQAS 538
Db 481 PLAGLDMDTFDSGFGVSGDCSSPVECDFTSPGDEGPPRSYLRQWVVI PPLSSPGPQAS 538

RESULT 4
PCT-US02-34502-16
; Sequence 16, Application PC/TUS0234502
; GENERAL INFORMATION:
; APPLICANT: ZymoGenetics, Inc.
; TITLE OF INVENTION: ZALPHALL LIGAND ANTAGONISTS
; FILE REFERENCE: 01-37PC
; CURRENT APPLICATION NUMBER: PCT/US02/34502
; CURRENT FILING DATE: 2002-10-28
; PRIOR APPLICATION NUMBER: 60/337,586
; PRIOR FILING DATE: 2001-11-05
; NUMBER OF SEQ ID NOS: 30
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 16
; LENGTH: 538
; TYPE: PRT
; ORGANISM: Homo sapiens
PCT-US02-34502-16
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Query Match 100.0%; Score 2958; DB 1; Length 538;
Best Local Similarity 100.0%; Pred. No. 1.5e-236;
Matches 538; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MPRGWAAPLLLLLQGGWGCEDLVCTYDTYLTQVICILEMNNLHPSTLTLTWQDOYEELKD 60
Db 1 MPRGWAAPLLLLLQGGWGCEDLVCTYDTYLTQVICILEMNNLHPSTLTLTWQDOYEELKD 60
Qy 61 EATCSLHRSAHNATHATYTTCHMDVHFHMADDIFSVNITDQSGNYSCGCSFLLAESIKP 120
Db 61 EATCSLHRSAHNATHATYTTCHMDVHFHMADDIFSVNITDQSGNYSCGCSFLLAESIKP 120
Qy 121 APPFNVTTFSGQYNISWRSYEDPAFYMLKGKQLQYELQYRNRGDPWAVSPRRKLISVDS 180
Db 121 APPFNVTTFSGQYNISWRSYEDPAFYMLKGKQLQYELQYRNRGDPWAVSPRRKLISVDS 180
Qy 181 RSVSLLPLEFRKDSSEYELQVRAGMPGSSYGQGTWSEWSDPVI FQTQSEELKEGWNPHLLL 240
Db 181 RSVSLLPLEFRKDSSEYELQVRAGMPGSSYGQGTWSEWSDPVI FQTQSEELKEGWNPHLLL 240
Qy 241 LLLLVIVIFAPFWSLKTPLWRLWKIWA VPSPERFPMPLYKCGSDGFKWVGAPFTGSS 300
Db 241 LLLLVIVIFAPFWSLKTPLWRLWKIWA VPSPERFPMPLYKCGSDGFKWVGAPFTGSS 300
Qy 301 LELGWPSEVPSTLEVSYCHPPSPAKRLQLTELQEPALVESDGVKPKSPFWPTAQNCGG 360
Db 301 LELGWPSEVPSTLEVSYCHPPSPAKRLQLTELQEPALVESDGVKPKSPFWPTAQNCGG 360
Qy 421 LLLLVIVIFAPFWSLKTPLWRLWKIWA VPSPERFPMPLYKCGSDGFKWVGAPFTGSS 480
Db 421 LLLLVIVIFAPFWSLKTPLWRLWKIWA VPSPERFPMPLYKCGSDGFKWVGAPFTGSS 480
Qy 481 SAYSEERDRPYGLVSDITVTVLDAEGPCTWPCSCEDDGYPALDLDAGLEPSPGLEDPILLD 538
Db 481 SAYSEERDRPYGLVSDITVTVLDAEGPCTWPCSCEDDGYPALDLDAGLEPSPGLEDPILLD 538
Qy 421 AGTTVLSGCGVSAGSPGLGGPLGSLDLRLKPLADGEDWAGGLPWGGRSPGCVSSEAGS 480
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Db 421 AGTTVLSGCGVSAGSPGLGGPLGSLDLRLKPLADGEDWAGGLPWGGRSPGCVSSEAGS 480
Qy 481 PLAGLDMDTFDSGFGVSGDCSSPVECDFTSPGDEGPPRSYLRQWVVI PPLSSPGPQAS 538
Db 481 PLAGLDMDTFDSGFGVSGDCSSPVECDFTSPGDEGPPRSYLRQWVVI PPLSSPGPQAS 538

RESULT 5
PCT-US03-17808-6
; Sequence 6, Application PC/TUS0317808
; GENERAL INFORMATION:
; APPLICANT: ZymoGenetics, Inc.
; APPLICANT: Nelson, Andrew J.
; APPLICANT: Hughes, Steven D.
; APPLICANT: Holly, Richard D.
; APPLICANT: Kindsvogel, Wayne R.
; TITLE OF INVENTION: USE OF IL-21 IN CANCER AND
; TITLE OF INVENTION: OTHER THERAPEUTIC APPLICATIONS
; FILE REFERENCE: 02-11PC
; CURRENT APPLICATION NUMBER: PCT/US03/17808
; CURRENT FILING DATE: 2003-06-06
; PRIOR APPLICATION NUMBER: US 60/387,127
; PRIOR FILING DATE: 2002-06-07
; NUMBER OF SEQ ID NOS: 17
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 6
; LENGTH: 538
; TYPE: PRT
; ORGANISM: Homo sapiens
PCT-US03-17808-6
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Query Match 100.0%; Score 2958; DB 1; Length 538;
Best Local Similarity 100.0%; Pred. No. 1.5e-236;
Matches 538; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MPRGWAAPLLLLLQGGWGCEDLVCTYDTYLTQVICILEMNNLHPSTLTLTWQDOYEELKD 60
Db 1 MPRGWAAPLLLLLQGGWGCEDLVCTYDTYLTQVICILEMNNLHPSTLTLTWQDOYEELKD 60
Qy 61 EATCSLHRSAHNATHATYTTCHMDVHFHMADDIFSVNITDQSGNYSCGCSFLLAESIKP 120
Db 61 EATCSLHRSAHNATHATYTTCHMDVHFHMADDIFSVNITDQSGNYSCGCSFLLAESIKP 120
Qy 121 APPFNVTTFSGQYNISWRSYEDPAFYMLKGKQLQYELQYRNRGDPWAVSPRRKLISVDS 180
Db 121 APPFNVTTFSGQYNISWRSYEDPAFYMLKGKQLQYELQYRNRGDPWAVSPRRKLISVDS 180
Qy 181 RSVSLLPLEFRKDSSEYELQVRAGMPGSSYGQGTWSEWSDPVI FQTQSEELKEGWNPHLLL 240
Db 181 RSVSLLPLEFRKDSSEYELQVRAGMPGSSYGQGTWSEWSDPVI FQTQSEELKEGWNPHLLL 240
Qy 241 LLLLVIVIFAPFWSLKTPLWRLWKIWA VPSPERFPMPLYKCGSDGFKWVGAPFTGSS 300
Db 241 LLLLVIVIFAPFWSLKTPLWRLWKIWA VPSPERFPMPLYKCGSDGFKWVGAPFTGSS 300
Qy 301 LELGWPSEVPSTLEVSYCHPPSPAKRLQLTELQEPALVESDGVKPKSPFWPTAQNCGG 360
Db 301 LELGWPSEVPSTLEVSYCHPPSPAKRLQLTELQEPALVESDGVKPKSPFWPTAQNCGG 360
Qy 361 SAYSEERDRPYGLVSDITVTVLDAEGPCTWPCSCEDDGYPALDLDAGLEPSPGLEDPILLD 420
Db 361 SAYSEERDRPYGLVSDITVTVLDAEGPCTWPCSCEDDGYPALDLDAGLEPSPGLEDPILLD 420
Qy 421 AGTTVLSGCGVSAGSPGLGGPLGSLDLRLKPLADGEDWAGGLPWGGRSPGCVSSEAGS 480
Db 421 AGTTVLSGCGVSAGSPGLGGPLGSLDLRLKPLADGEDWAGGLPWGGRSPGCVSSEAGS 480
Qy 481 PLAGLDMDTFDSGFGVSGDCSSPVECDFTSPGDEGPPRSYLRQWVVI PPLSSPGPQAS 538
Db 481 PLAGLDMDTFDSGFGVSGDCSSPVECDFTSPGDEGPPRSYLRQWVVI PPLSSPGPQAS 538

RESULT 6
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PCT-US03-21975-4
; Sequence 4, Application PC/TUS0321975
; GENERAL INFORMATION:
; APPLICANT: Wyeth
; APPLICANT: Grusby, Michael J
; APPLICANT: Wurster, Andrea
; APPLICANT: Young, Deborah
; APPLICANT: Collins, Mary
; APPLICANT: Whitters, Matthew
; TITLE OF INVENTION: Methods and Compositions for Modulating T Helper (TH)
; FILE REFERENCE: 22058-585-061
; CURRENT APPLICATION NUMBER: PCT/US03/21975
; CURRENT FILING DATE: 2003-07-15
; PRIOR APPLICATION NUMBER: 60/396,160
; PRIOR FILING DATE: 2002-07-15
; PRIOR APPLICATION NUMBER: 60/403,001
; PRIOR FILING DATE: 2002-08-12
; NUMBER OF SEQ ID NOS: 13
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 4
; LENGTH: 538
; TYPE: PRT
; ORGANISM: Homo sapiens
PCT-US03-21975-4

Query Match 100.0%; Score 2958; DB 1; Length 538;
Best Local Similarity 100.0%; Pred. No. 1.5e-236;
Matches 538; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MPRGWAAPLILLLQGGWCPDLVCYTDYLTQVICILEMNLHPSTLTWTQOYBELKD 60
Db 1 MPRGWAAPLILLLQGGWCPDLVCYTDYLTQVICILEMNLHPSTLTWTQOYBELKD 60

Qy 61 EATCSLHRSAHNATHATYTCMDVHFHMADDIFSVNITDQSGNYSQECGSFLAESIKP 120
Db 61 EATCSLHRSAHNATHATYTCMDVHFHMADDIFSVNITDQSGNYSQECGSFLAESIKP 120

Qy 121 APPFNVTFTSGQYNIWSRSDYEDPAFYMLKGKLOYELQYLRNRGDPWAVSPRKLISVDS 180
Db 121 APPFNVTFTSGQYNIWSRSDYEDPAFYMLKGKLOYELQYLRNRGDPWAVSPRKLISVDS 180

Qy 181 RSVSLPLERFKOSSYELQVRAGMPGSSYQGTWSEWSDPVIQTQSEELKEGWNPHLL 240
Db 181 RSVSLPLERFKOSSYELQVRAGMPGSSYQGTWSEWSDPVIQTQSEELKEGWNPHLL 240

Qy 241 LLLLVIVIFAPFWSLKTPLWRLWKKIWAVSPERFMPYKGCSDGFKKWVGAPFTGSS 300
Db 241 LLLLVIVIFAPFWSLKTPLWRLWKKIWAVSPERFMPYKGCSDGFKKWVGAPFTGSS 300

Qy 301 LELGWPSPVPSTLEVYSCHPSPAKRLQTLQEPAEELVESDGVKPSFWPTAQNSSG 360
Db 301 LELGWPSPVPSTLEVYSCHPSPAKRLQTLQEPAEELVESDGVKPSFWPTAQNSSG 360

Qy 361 SAYSEERDRPYGLVSIIDTVTLDAEGCTWPCSCDDGYPALDLADGLESPGLDPLLD 420
Db 361 SAYSEERDRPYGLVSIIDTVTLDAEGCTWPCSCDDGYPALDLADGLESPGLDPLLD 420

Qy 421 AGTTVLSGCVSAGSPGLGGPLGSLDLRLKPLADGEDWAGGLPWGGRSPGVSESEAGS 480
Db 421 AGTTVLSGCVSAGSPGLGGPLGSLDLRLKPLADGEDWAGGLPWGGRSPGVSESEAGS 480

Qy 481 PLAGLMDTDFSGVSGDCSSPVECDFTSPGDEGPPRSYLRQWVVIPTPLSSPGPQAS 538
Db 481 PLAGLMDTDFSGVSGDCSSPVECDFTSPGDEGPPRSYLRQWVVIPTPLSSPGPQAS 538

RESULT 7
PCT-US04-08833-6
; Sequence 6, Application PC/TUS0408833
; GENERAL INFORMATION:
; APPLICANT: Wyeth
; TITLE OF INVENTION: TREATING IMMUNOLOGICAL DISORDERS USING AGONISTS OF

; TITLE OF INVENTION: INTERLEUKIN-21/ INTERLEUKIN-21 RECEPTOR
; FILE REFERENCE: 16158-013W01
; CURRENT APPLICATION NUMBER: PCT/US04/08833
; CURRENT FILING DATE: 2004-03-26
; PRIOR APPLICATION NUMBER: US 60/456,920
; PRIOR FILING DATE: 2003-03-21
; NUMBER OF SEQ ID NOS: 13
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 6
; LENGTH: 538
; TYPE: PRT
; ORGANISM: Homo sapiens
PCT-US04-08833-6

Query Match 100.0%; Score 2958; DB 1; Length 538;
Best Local Similarity 100.0%; Pred. No. 1.5e-236;
Matches 538; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MPRGWAAPLILLLQGGWCPDLVCYTDYLTQVICILEMNLHPSTLTWTQOYBELKD 60
Db 1 MPRGWAAPLILLLQGGWCPDLVCYTDYLTQVICILEMNLHPSTLTWTQOYBELKD 60

Qy 61 EATCSLHRSAHNATHATYTCMDVHFHMADDIFSVNITDQSGNYSQECGSFLAESIKP 120
Db 61 EATCSLHRSAHNATHATYTCMDVHFHMADDIFSVNITDQSGNYSQECGSFLAESIKP 120

Qy 121 APPFNVTFTSGQYNIWSRSDYEDPAFYMLKGKLOYELQYLRNRGDPWAVSPRKLISVDS 180
Db 121 APPFNVTFTSGQYNIWSRSDYEDPAFYMLKGKLOYELQYLRNRGDPWAVSPRKLISVDS 180

Qy 181 RSVSLPLERFKOSSYELQVRAGMPGSSYQGTWSEWSDPVIQTQSEELKEGWNPHLL 240
Db 181 RSVSLPLERFKOSSYELQVRAGMPGSSYQGTWSEWSDPVIQTQSEELKEGWNPHLL 240

Qy 241 LLLLVIVIFAPFWSLKTPLWRLWKKIWAVSPERFMPYKGCSDGFKKWVGAPFTGSS 300
Db 241 LLLLVIVIFAPFWSLKTPLWRLWKKIWAVSPERFMPYKGCSDGFKKWVGAPFTGSS 300

Qy 301 LELGWPSPVPSTLEVYSCHPSPAKRLQTLQEPAEELVESDGVKPSFWPTAQNSSG 360
Db 301 LELGWPSPVPSTLEVYSCHPSPAKRLQTLQEPAEELVESDGVKPSFWPTAQNSSG 360

Qy 361 SAYSEERDRPYGLVSIIDTVTLDAEGCTWPCSCDDGYPALDLADGLESPGLDPLLD 420
Db 361 SAYSEERDRPYGLVSIIDTVTLDAEGCTWPCSCDDGYPALDLADGLESPGLDPLLD 420

Qy 421 AGTTVLSGCVSAGSPGLGGPLGSLDLRLKPLADGEDWAGGLPWGGRSPGVSESEAGS 480
Db 421 AGTTVLSGCVSAGSPGLGGPLGSLDLRLKPLADGEDWAGGLPWGGRSPGVSESEAGS 480

Qy 481 PLAGLMDTDFSGVSGDCSSPVECDFTSPGDEGPPRSYLRQWVVIPTPLSSPGPQAS 538
Db 481 PLAGLMDTDFSGVSGDCSSPVECDFTSPGDEGPPRSYLRQWVVIPTPLSSPGPQAS 538

RESULT 8
US-09-159-254-2
; Sequence 2, Application US/09159254
; GENERAL INFORMATION:
; APPLICANT: Fresnell, Scott R.
; APPLICANT: Conklin, Darrell C.
; APPLICANT: Parrish, Julia E.
; APPLICANT: Hammond, Angela K.
; TITLE OF INVENTION: Cytokine receptor zalphail
; FILE REFERENCE: 98-55X
; CURRENT APPLICATION NUMBER: US/09/159,254
; CURRENT FILING DATE: 1998-09-23
; NUMBER OF SEQ ID NOS: 23
; SOFTWARE: Fast-SEQ for Windows Version 3.0
; SEQ ID NO 2
; LENGTH: 538
; TYPE: PRT
; ORGANISM: Homo sapiens

US-09-159-254-2

Query Match 100.0%; Score 2958; DB 15; Length 538;
Best Local Similarity 100.0%; Pred. No. 1.5e-236;
Matches 538; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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QY 1 MPRGWAAPLLLLLQGGWGPCDPLVCYTDYLTQTVICILEMNNLHPSTLTTLTWQDQYEELKD 60
Db 1 MPRGWAAPLLLLLQGGWGPCDPLVCYTDYLTQTVICILEMNNLHPSTLTTLTWQDQYEELKD 60
QY 61 EATCSLHRSAHNATHATYTCMDVHFHMADDIFSVNITDQSGNYSQECGSLFLAESIKP 120
Db 61 EATCSLHRSAHNATHATYTCMDVHFHMADDIFSVNITDQSGNYSQECGSLFLAESIKP 120
QY 121 APPFNVTTFSGQYNISWRSDYEDPAFYMLKGKLYELQYRNRPDPAVSPRRKLISVDS 180
Db 121 APPFNVTTFSGQYNISWRSDYEDPAFYMLKGKLYELQYRNRPDPAVSPRRKLISVDS 180
QY 181 RSVSLPLPLEFRKDSSEYELQVRAGMPGSSYQGTWSEWSDPVIQTQSEBELKEGWNPHLLL 240
Db 181 RSVSLPLPLEFRKDSSEYELQVRAGMPGSSYQGTWSEWSDPVIQTQSEBELKEGWNPHLLL 240
QY 241 LLLLVIPIPAFWSLKTPLWRLWKKIWAVSPERFFMPLYKGCSDGDFKKWVGAPFTGSS 300
Db 241 LLLLVIPIPAFWSLKTPLWRLWKKIWAVSPERFFMPLYKGCSDGDFKKWVGAPFTGSS 300
QY 301 LELGWSPEVPSTLEVYSCHPPRSPAKRLQLTELQEPALVESDGVKPSFWPTAQNSGG 360
Db 301 LELGWSPEVPSTLEVYSCHPPRSPAKRLQLTELQEPALVESDGVKPSFWPTAQNSGG 360
QY 361 SAYSEERDRPYGLVSDITVTVDAGPCTWPCSCDDGYPALDDAGLESPGLEDDPLLD 420
Db 361 SAYSEERDRPYGLVSDITVTVDAGPCTWPCSCDDGYPALDDAGLESPGLEDDPLLD 420
QY 421 AGTTVLSCGCVSAGSPGLGGPLGSLDLRLKPLADGEDWAGGLPWGGRSPGVSVSEAGS 480
Db 421 AGTTVLSCGCVSAGSPGLGGPLGSLDLRLKPLADGEDWAGGLPWGGRSPGVSVSEAGS 480
QY 481 PLAGLDMDTFDSGFGVSDCSSPVECDFTSPGDEGPPRSYLRQWVVIPLPSSPGPQAS 538
Db 481 PLAGLDMDTFDSGFGVSDCSSPVECDFTSPGDEGPPRSYLRQWVVIPLPSSPGPQAS 538
```

RESULT 9

US-09-264-908-2

; Sequence 2, Application US/09264908

; GENERAL INFORMATION:

; APPLICANT: Parrish, Julia E.

; APPLICANT: Hammond, Angela K.

; APPLICANT: Presnell, Scott R.

; APPLICANT: Sprecher, Cindy A.

; APPLICANT: Gross, Jane A.

; APPLICANT: Johnston, Janet V.

; APPLICANT: Xu, Wen-feng

; APPLICANT: Grant, Francis J.

; APPLICANT: Foster, Donald C.

; APPLICANT: Kuijper, Joseph L.

; TITLE OF INVENTION: NOVEL CYTOKINE ZALPHA11 LIGAND

; FILE REFERENCE: 99-16X

; CURRENT APPLICATION NUMBER: US/09/264,908

; CURRENT FILING DATE: 1999-03-09

; NUMBER OF SEQ ID NOS: 49

; SOFTWARE: FastSeq for Windows Version 3.0

; SEQ ID NO 2

; LENGTH: 538

; TYPE: PRT

; ORGANISM: Homo sapiens

US-09-264-908-2

Query Match 100.0%; Score 2958; DB 16; Length 538;
Best Local Similarity 100.0%; Pred. No. 1.5e-236;
Matches 538; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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QY 1 MPRGWAAPLLLLLQGGWGPCDPLVCYTDYLTQTVICILEMNNLHPSTLTTLTWQDQYEELKD 60
Db 1 MPRGWAAPLLLLLQGGWGPCDPLVCYTDYLTQTVICILEMNNLHPSTLTTLTWQDQYEELKD 60
QY 61 EATCSLHRSAHNATHATYTCMDVHFHMADDIFSVNITDQSGNYSQECGSLFLAESIKP 120
Db 61 EATCSLHRSAHNATHATYTCMDVHFHMADDIFSVNITDQSGNYSQECGSLFLAESIKP 120
QY 121 APPFNVTTFSGQYNISWRSDYEDPAFYMLKGKLYELQYRNRPDPAVSPRRKLISVDS 180
Db 121 APPFNVTTFSGQYNISWRSDYEDPAFYMLKGKLYELQYRNRPDPAVSPRRKLISVDS 180
QY 181 RSVSLPLPLEFRKDSSEYELQVRAGMPGSSYQGTWSEWSDPVIQTQSEBELKEGWNPHLLL 240
Db 181 RSVSLPLPLEFRKDSSEYELQVRAGMPGSSYQGTWSEWSDPVIQTQSEBELKEGWNPHLLL 240
QY 241 LLLLVIPIPAFWSLKTPLWRLWKKIWAVSPERFFMPLYKGCSDGDFKKWVGAPFTGSS 300
Db 241 LLLLVIPIPAFWSLKTPLWRLWKKIWAVSPERFFMPLYKGCSDGDFKKWVGAPFTGSS 300
QY 301 LELGWSPEVPSTLEVYSCHPPRSPAKRLQLTELQEPALVESDGVKPSFWPTAQNSGG 360
Db 301 LELGWSPEVPSTLEVYSCHPPRSPAKRLQLTELQEPALVESDGVKPSFWPTAQNSGG 360
QY 361 SAYSEERDRPYGLVSDITVTVDAGPCTWPCSCDDGYPALDDAGLESPGLEDDPLLD 420
Db 361 SAYSEERDRPYGLVSDITVTVDAGPCTWPCSCDDGYPALDDAGLESPGLEDDPLLD 420
QY 421 AGTTVLSCGCVSAGSPGLGGPLGSLDLRLKPLADGEDWAGGLPWGGRSPGVSVSEAGS 480
Db 421 AGTTVLSCGCVSAGSPGLGGPLGSLDLRLKPLADGEDWAGGLPWGGRSPGVSVSEAGS 480
QY 481 PLAGLDMDTFDSGFGVSDCSSPVECDFTSPGDEGPPRSYLRQWVVIPLPSSPGPQAS 538
Db 481 PLAGLDMDTFDSGFGVSDCSSPVECDFTSPGDEGPPRSYLRQWVVIPLPSSPGPQAS 538
```

RESULT 10

US-09-265-117-2

; Sequence 2, Application US/09265117

; GENERAL INFORMATION:

; APPLICANT: Presnell, Scott R.

; APPLICANT: Conklin, Darrell C.

; APPLICANT: Parrish, Julia E.

; APPLICANT: Hammond, Angela K.

; TITLE OF INVENTION: CYTOKINE RECEPTOR ZALPHA11

; FILE REFERENCE: 98-55X2

; CURRENT APPLICATION NUMBER: US/09/265,117

; CURRENT FILING DATE: 1999-03-09

; NUMBER OF SEQ ID NOS: 49

; SOFTWARE: FastSeq for Windows Version 3.0

; SEQ ID NO 2

; LENGTH: 538

; TYPE: PRT

; ORGANISM: Homo sapiens

US-09-265-117-2

Query Match 100.0%; Score 2958; DB 16; Length 538;
Best Local Similarity 100.0%; Pred. No. 1.5e-236;
Matches 538; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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QY 1 MPRGWAAPLLLLLQGGWGPCDPLVCYTDYLTQTVICILEMNNLHPSTLTTLTWQDQYEELKD 60
Db 1 MPRGWAAPLLLLLQGGWGPCDPLVCYTDYLTQTVICILEMNNLHPSTLTTLTWQDQYEELKD 60
QY 61 EATCSLHRSAHNATHATYTCMDVHFHMADDIFSVNITDQSGNYSQECGSLFLAESIKP 120
Db 61 EATCSLHRSAHNATHATYTCMDVHFHMADDIFSVNITDQSGNYSQECGSLFLAESIKP 120
QY 121 APPFNVTTFSGQYNISWRSDYEDPAFYMLKGKLYELQYRNRPDPAVSPRRKLISVDS 180
Db 121 APPFNVTTFSGQYNISWRSDYEDPAFYMLKGKLYELQYRNRPDPAVSPRRKLISVDS 180
```


RESULT 13

US-09-543-320-2
; Sequence 2, Application US/09543320
; GENERAL INFORMATION:
; APPLICANT: Sprecher, Cindy A.
; APPLICANT: Brandt, Cameron S.
; APPLICANT: West, James W.
; TITLE OF INVENTION: SOLUBLE ZALPHA11 CYTOKINE RECEPTORS
; FILE REFERENCE: 00-22X
; CURRENT APPLICATION NUMBER: US/09/543,320
; CURRENT FILING DATE: 2000-04-05
; NUMBER OF SEQ ID NOS: 63
; SOFTWARE: FASTSEQ for Windows Version 3.0
; SEQ ID NO 2
; LENGTH: 538
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-543-320-2

Query Match 100.0%; Score 2958; DB 19; Length 538;
Best Local Similarity 100.0%; Pred. No. 1.5e-236;
Matches 538; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MPRGWAAPLLLLLLGGGCGPDLVCYTDYLTQVVICILEMNLHPSTLTLTWQDQYEELKD 60
DB 1 MPRGWAAPLLLLLLGGGCGPDLVCYTDYLTQVVICILEMNLHPSTLTLTWQDQYEELKD 60

QY 61 EATCSLHRSAHNATHATTCHMDVHFHMADDIFSVNITDQSGNYSOEGSFLAESTKP 120
DB 61 EATCSLHRSAHNATHATTCHMDVHFHMADDIFSVNITDQSGNYSOEGSFLAESTKP 120

QY 121 APPFNVTTFSGQYNISWRSDYEDPAFYMKGKQLQYELQYRNRPDPAVSPRKLISVDS 180
DB 121 APPFNVTTFSGQYNISWRSDYEDPAFYMKGKQLQYELQYRNRPDPAVSPRKLISVDS 180

QY 181 RVSLLPLEFRKDSSEYELQVRAGMPGSSYQGTWSESDPVIQTQSEBELKEGWNPHLLL 240
DB 181 RVSLLPLEFRKDSSEYELQVRAGMPGSSYQGTWSESDPVIQTQSEBELKEGWNPHLLL 240

QY 241 LLLLVIVFIPAFWSLTKTHPLRLKTIWAVSPERFPMPLKYGCSGDFKKWVGAPFTGSS 300
DB 241 LLLLVIVFIPAFWSLTKTHPLRLKTIWAVSPERFPMPLKYGCSGDFKKWVGAPFTGSS 300

QY 301 LELGWSPEVSTLEVSCHPPSPAKRLQLTELQEPALVELSDGVKPSFWPTAQNSSG 360
DB 301 LELGWSPEVSTLEVSCHPPSPAKRLQLTELQEPALVELSDGVKPSFWPTAQNSSG 360

QY 361 SAYSEERDRPYGLVSDITVTVLDAEGPCTWPCSCDDGYPALDLDAGLEPSPGLDPLLD 420
DB 361 SAYSEERDRPYGLVSDITVTVLDAEGPCTWPCSCDDGYPALDLDAGLEPSPGLDPLLD 420

QY 421 AGTTVLSGCVSAGSPGLGGPLGSLDLRLKPLADGEDWAGGLPWGGRSPGVSSSEAGS 480
DB 421 AGTTVLSGCVSAGSPGLGGPLGSLDLRLKPLADGEDWAGGLPWGGRSPGVSSSEAGS 480

QY 481 PLAGLDMDTFDSGFVSGDCSSPVECDFTSPGDEGPPRSYLRQWVIPPPLSSPGQAS 538
DB 481 PLAGLDMDTFDSGFVSGDCSSPVECDFTSPGDEGPPRSYLRQWVIPPPLSSPGQAS 538

RESULT 14

US-09-560-766-2
; Sequence 2, Application US/09560766
; GENERAL INFORMATION:
; APPLICANT: Donaldson, Debra
; APPLICANT: Unger, Michelle
; TITLE OF INVENTION: MU-1 RECEPTOR
; NUMBER OF SEQUENCES: 8
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Genetics Institute, Inc.
; STREET: 87 CambridgePark Drive

CITY: Cambridge
STATE: MA
COUNTRY: USA
ZIP: 02140
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/560,766
FILING DATE:
CLASSIFICATION:
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/560,766
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Brown, Scott A
REGISTRATION NUMBER: 32,724
REFERENCE/DOCKET NUMBER: G15320
TELECOMMUNICATION INFORMATION:
TELEPHONE: 617-498-8224
TELEFAX: 617-876-5851
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 538 amino acids
TYPE: amino acid
STRANDEDNESS:
TOPOLOGY: linear
MOLECULE TYPE: protein
US-09-560-766-2

Query Match 100.0%; Score 2958; DB 19; Length 538;
Best Local Similarity 100.0%; Pred. No. 1.5e-236;
Matches 538; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MPRGWAAPLLLLLLGGGCGPDLVCYTDYLTQVVICILEMNLHPSTLTLTWQDQYEELKD 60
DB 1 MPRGWAAPLLLLLLGGGCGPDLVCYTDYLTQVVICILEMNLHPSTLTLTWQDQYEELKD 60

QY 61 EATCSLHRSAHNATHATTCHMDVHFHMADDIFSVNITDQSGNYSOEGSFLAESTKP 120
DB 61 EATCSLHRSAHNATHATTCHMDVHFHMADDIFSVNITDQSGNYSOEGSFLAESTKP 120

QY 121 APPFNVTTFSGQYNISWRSDYEDPAFYMKGKQLQYELQYRNRPDPAVSPRKLISVDS 180
DB 121 APPFNVTTFSGQYNISWRSDYEDPAFYMKGKQLQYELQYRNRPDPAVSPRKLISVDS 180

QY 181 RVSLLPLEFRKDSSEYELQVRAGMPGSSYQGTWSESDPVIQTQSEBELKEGWNPHLLL 240
DB 181 RVSLLPLEFRKDSSEYELQVRAGMPGSSYQGTWSESDPVIQTQSEBELKEGWNPHLLL 240

QY 241 LLLLVIVFIPAFWSLTKTHPLRLKTIWAVSPERFPMPLKYGCSGDFKKWVGAPFTGSS 300
DB 241 LLLLVIVFIPAFWSLTKTHPLRLKTIWAVSPERFPMPLKYGCSGDFKKWVGAPFTGSS 300

QY 301 LELGWSPEVSTLEVSCHPPSPAKRLQLTELQEPALVELSDGVKPSFWPTAQNSSG 360
DB 301 LELGWSPEVSTLEVSCHPPSPAKRLQLTELQEPALVELSDGVKPSFWPTAQNSSG 360

QY 361 SAYSEERDRPYGLVSDITVTVLDAEGPCTWPCSCDDGYPALDLDAGLEPSPGLDPLLD 420
DB 361 SAYSEERDRPYGLVSDITVTVLDAEGPCTWPCSCDDGYPALDLDAGLEPSPGLDPLLD 420

QY 421 AGTTVLSGCVSAGSPGLGGPLGSLDLRLKPLADGEDWAGGLPWGGRSPGVSSSEAGS 480
DB 421 AGTTVLSGCVSAGSPGLGGPLGSLDLRLKPLADGEDWAGGLPWGGRSPGVSSSEAGS 480

QY 481 PLAGLDMDTFDSGFVSGDCSSPVECDFTSPGDEGPPRSYLRQWVIPPPLSSPGQAS 538
DB 481 PLAGLDMDTFDSGFVSGDCSSPVECDFTSPGDEGPPRSYLRQWVIPPPLSSPGQAS 538

RESULT 15

US-09-569-384-2
; Sequence 2, Application US/09569384
; GENERAL INFORMATION:
; APPLICANT: Donaldson, Deborah
; APPLICANT: Unger, Michelle
; APPLICANT: Collins, Mary
; APPLICANT: Whitters, Matthew J.
; APPLICANT: Lowe, Leslie
; APPLICANT: Young, Deborah A.
; TITLE OF INVENTION: MU-1, MEMBER OF THE CYTOKINE RECEPTOR FAMILY
; FILE REFERENCE: GEN-5230CP
; CURRENT APPLICATION NUMBER: US/09/569,384
; CURRENT FILING DATE: 2000-05-11
; PRIOR APPLICATION NUMBER: 09/040,005
; PRIOR FILING DATE: 1998-03-17
; NUMBER OF SEQ ID NOS: 16
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 2
; LENGTH: 538
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-569-384-2

Query Match 100.0%; Score 2958; DB 19; Length 538;
Best Local Similarity 100.0%; Pred. No. 1.5e-236;
Matches 538; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MPRGWAAPLLLLLLGGGCGCDPLVCYTDYLOTVICILEMNNLHPSTLTLTWQDQYEELKD 60
DB 1 MPRGWAAPLLLLLLGGGCGCDPLVCYTDYLOTVICILEMNNLHPSTLTLTWQDQYEELKD 60

QY 61 EATCSLHSAHNATHATYTCMDFHEWADDIFSVNITDQSGNYSCGSGFLAESIKP 120
DB 61 EATCSLHSAHNATHATYTCMDFHEWADDIFSVNITDQSGNYSCGSGFLAESIKP 120

QY 121 APPFNVTTFSGQYNISNRSDYEDPAFYMLKGKQLQYELQYRNRGDPWAVSPRKLISYDS 180
DB 121 APPFNVTTFSGQYNISNRSDYEDPAFYMLKGKQLQYELQYRNRGDPWAVSPRKLISYDS 180

QY 181 RSVSLLPLEFRKDSYELQVRAGMPGSSYQGTWSESDPVIQTQSEELKEGWNPHLLL 240
DB 181 RSVSLLPLEFRKDSYELQVRAGMPGSSYQGTWSESDPVIQTQSEELKEGWNPHLLL 240

QY 241 LLLLVIIVFIPAFWSLTKTHPLMKKIWAVSPERFPMPLKYGCSGDFKKWVGAPFTGSS 300
DB 241 LLLLVIIVFIPAFWSLTKTHPLMKKIWAVSPERFPMPLKYGCSGDFKKWVGAPFTGSS 300

QY 301 LELGPWSPVPSTLEVYSCHPSPSPAKRIQLTELQEPALVESDGVKPSFWPTAQNSGG 360
DB 301 LELGPWSPVPSTLEVYSCHPSPSPAKRIQLTELQEPALVESDGVKPSFWPTAQNSGG 360

QY 361 SAYSEERDRPYGLVIDITVTLVLDAGGCTWPCSCDDGYPALDL DAGLEPSPGLEDPDLLD 420
DB 361 SAYSEERDRPYGLVIDITVTLVLDAGGCTWPCSCDDGYPALDL DAGLEPSPGLEDPDLLD 420

QY 421 AGTTVLSCGCVSAGSPGLGSLDLRLKPLADGEDWAGGLPWGGRSPGCVSESEAGS 480
DB 421 AGTTVLSCGCVSAGSPGLGSLDLRLKPLADGEDWAGGLPWGGRSPGCVSESEAGS 480

QY 481 PLAGLDMDTFDSGFVSGDCSSPVECDFTSPGDEGPPRSYLRQWVVI PPLSSPGFQAS 538
DB 481 PLAGLDMDTFDSGFVSGDCSSPVECDFTSPGDEGPPRSYLRQWVVI PPLSSPGFQAS 538

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Job time : 478 secs